

60110USPCT1 Corrected SEQ LIST 2-2007.txt
SEQUENCE LISTING



<110> Lanahan, Mike

<120> Self-processing Plants and Plant Parts

<130> 109846.317

<140> PCT/US04/07182

<141> 2004-03-15

<160> 112

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1

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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
115 120 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130 135 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145 150 155 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
165 170 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180 185 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
195 200 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
210 215 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225 230 235 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
245 250 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
260 265 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
275 280 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
290 295 300

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Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305 310 315 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
325 330 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
340 345 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
355 360 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
370 375 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385 390 395 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
405 410 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
420 425 430
Cys Gly Val Gly
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<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

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gccggcatct cgcgcattctg gataccgcca gcttccaagg gcatgtccgg gggctactcg 180
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gagacgcgt tcgggtccaa gcaggagtc atcaacatga tcaacacggc gcacgcctac 300
ggcatcaagg tcatcgcgga catcgatc aaccacaggg ccggcggcga cctggagtgg 360
aacccgttcg tcggcgacta caccctggacg gacttctcca aggtcgccctc cggcaagtac 420
accgccaact acctcgactt ccaccccaac gagctgcacg cgggcgactc cggcacgttc 480
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gtgggcgagt actgggacac caacgtcgac ggcgtgctca actgggccta ctcctccggc 720
gccaagggtt tcgacttccc cctgtactac aagatggacg cggccttcga caacaagaac 780
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<211> 800
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

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 Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala Lys Asp Val
 35 40 45
 Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala Glu Val Trp
 50 55 60
 Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro Asp Thr Ser
 65 70 75 80
 Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val Ile Glu Ala
 85 90 95
 Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Glu Leu Phe Lys Val
 100 105 110
 Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu Lys Ala Asp
 115 120 125
 Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val Leu Ser Glu
 130 135 140
 Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu Ile Ile Glu
 145 150 155 160
 Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu Asp Asp Tyr
 165 170 175
 Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu Lys Thr Ile
 180 185 190
 Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val Leu Leu Phe
 195 200 205
 Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn Met Glu Tyr
 210 215 220
 Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp Leu Asp Gly
 225 230 235 240
 Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile Arg Thr Thr
 245 250 255
 Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln Glu Ser Ala
 260 265 270
 Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu Asn Asp Arg
 275 280 285
 Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr Glu Ile His
 290 295 300
 Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys Asn Lys Gly
 305 310 315 320
 Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Gly Pro Gly Gly Val
 325 330 335
 Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr His Val His
 340 345 350
 Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu Asp Lys Asp
 355 360 365
 Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu Phe Met Val
 370 375 380
 Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His Thr Arg Ile
 385 390 395 400
 Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His Gly Ile Gly
 405 410 415
 Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile Gly Glu Leu
 420 425 430
 Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg Ile Asp Lys
 435 440 445
 Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val Ile Ala Ser
 450 455 460
 Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val Thr Tyr Trp
 465 470 475 480
 Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln Met Gly Leu
 485 490 495
 Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu His Lys Ile
 500 505 510
 Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly Trp Gly Ala

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515	520	525
Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His Val Ala Ala		
530	535	540
Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val Phe Asn Pro		
545	550	555
Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu Thr Lys Ile		
565	570	575
Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys Leu Ile Lys		
580	585	590
Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala Ala Cys His		
595	600	605
Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala Lys Ala Asp		
610	615	620
Lys Lys Lys Glu Trp Thr Glu Glu Leu Lys Asn Ala Gln Lys Leu		
625	630	635
Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe Leu His Gly		
645	650	655
Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn Ser Tyr Asn		
660	665	670
Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys Leu Gln Phe		
675	680	685
Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu Arg Lys Glu		
690	695	700
His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys Lys His Leu		
705	710	715
Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met Leu Lys Asp		
725	730	735
His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile Tyr Asn Gly		
740	745	750
Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys Trp Asn Val		
755	760	765
Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu Thr Val Glu		
770	775	780
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<210> 4

<211> 2400

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 4

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gccgaggtgt ggatactcca gggcgtggag	gagatcttct acgagaagcc ggacacctcc	240
ccgcgcattt tcttcgcccc	ggcccgctcc aacaaggta tcgaggcctt cctcaccac	300
ccgggtggaca ccaagaagaa ggagctttc	aaggtgaccg tcgacggcaa ggagatccc	360
gtgtcccgcg tggagaaggc cgacccgacc	gacatcgacg tgaccaacta cgtgcgcattc	420
gtgctctccg agtccctcaa ggaggaggac	ctccgcaagg acgtggagct gatcatcgag	480
ggctacaagc cggcccgct	gatcatgatg gagatcctcg acgactacta ctacgacggc	540
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gttttctacc tctaccagct ggagaactac	ggcaagatcc gcaccaccgt ggaccctgtac	780
tccaaggccg tgtacgccaa caaccaggag	tctgcagtgg tgaacctcgc cggcaccaac	840
ccggagggtt gggagaacga cccggcccg	aagatcgagg gctacgagga cgccatcatc	900
tacgagatcc acatcgccga catcaccggc	ctggagaact ccggcgtgaa gaacaaggc	960
ctctacctcg gcctcaccga ggagaacacc	aaggccccgg gcggcgtgac caccggcctc	1020

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ctcttcatgg	tgccggaggg	ccgctactcc	accgaccgc	agaaccgc	cacccgaatt	1200
cgcgaggtga	aggagatgtt	gaaggccctc	cacaagcacg	gcatcggcgt	gatcatggac	1260
atggtgttcc	cgcacaccta	cggcatcggc	gagctgtccg	cttcgacca	gaccgtgccg	1320
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cacgtggccg	ccttcaacga	cgagttccgc	gacgccatcc	gcccgtccgt	gttcaacccg	1680
tccgtgaagg	gcttcgttat	gggcggctac	ggcaaggaga	ccaagatcaa	ggcgcggcgt	1740
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accatcaact	acgcccctg	ccacgacaac	cacaccctct	gggacaagaa	ctacctcgcc	1860
gccaaggccg	acaagaagaa	ggagtggacc	gaggaggagc	tgaagaacgc	ccagaagctc	1920
gccggcgcca	tcctcctcac	tagtcagggc	gtgccgttcc	tccacggcgg	ccaggacttc	1980
tgccgcacca	ccaacttcaa	cgacaactcc	tacaacgccc	cgatctccat	caacggcttc	2040
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gagttcctcc	cgggcggggcg	ccgcatcg	gccttcatgc	tcaaggacca	cgccggcggc	2220
gaccctgtgg	aggacatcgt	ggtgatctac	aacggcaacc	tggagaagac	cacctacaag	2280
ctcccggagg	gcaagtggaa	cgtggtggtg	aactcccaga	aggccggcac	cgaggtgatc	2340
gagaccgtgg	agggcaccat	cgagctggac	ccgctctccg	cctacgtgct	ctaccgcgag	2400

<210> 5

<211> 693

<212> PRT

<213> *Sulfolobus solfataricus*

<400> 5

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							20				25		30		
Ser	Ser	Asn	Lys	Ser	Leu	Ser	Glu	Leu	Gly	Leu	Thr	Ile	Val	Gln	Gln
							35			40		45			
Gly	Asn	Lys	Val	Ile	val	Glu	Lys	Ser	Leu	Asp	Leu	Lys	Glu	His	Ile
							50			55		60			
Ile	Gly	Leu	Gly	Glu	Lys	Ala	Phe	Glu	Leu	Asp	Arg	Lys	Arg	Lys	Arg
							65			70		75		80	
Tyr	Val	Met	Tyr	Asn	Val	Asp	Ala	Gly	Ala	Tyr	Lys	Lys	Tyr	Gln	Asp
							85			90		95			
Pro	Leu	Tyr	Val	Ser	Ile	Pro	Leu	Phe	Ile	Ser	Val	Lys	Asp	Gly	Val
							100			105		110			
Ala	Thr	Gly	Tyr	Phe	Phe	Asn	Ser	Ala	Ser	Lys	Val	Ile	Phe	Asp	Val
							115			120		125			
Gly	Leu	Glu	Glu	Tyr	Asp	Lys	Val	Ile	Val	Thr	Ile	Pro	Glu	Asp	Ser
							130			135		140			
Val	Glu	Phe	Tyr	Val	Ile	Glu	Gly	Pro	Arg	Ile	Glu	Asp	Val	Leu	Glu
							145			150		155		160	
Lys	Tyr	Thr	Glu	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Pro	Pro	Met	Trp	Ala
							165			170		175			
Phe	Gly	Tyr	Met	Ile	Ser	Arg	Tyr	Ser	Tyr	Tyr	Pro	Gln	Asp	Lys	Val
							180			185		190			
Val	Glu	Leu	Val	Asp	Ile	Met	Gln	Lys	Glu	Gly	Phe	Arg	Val	Ala	Gly
							195			200		205			
Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu	Phe	Thr	Trp
							210			215		220			
His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile	Asp	Glu	Leu	His
							225			230		235		240	
Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly	Ile	Arg	Val
							245			250		255			

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Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly	Lys	Phe	Cys	Glu
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Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp	Pro	Gly	Thr	Thr
	275						280				285				
Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp	Trp	Ala	Gly
	290					295				300					
Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile	Trp	Leu	Asp
	305					310			315					320	
Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu	Ile	Arg	Asp	Val
								325		330			335		
Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg	Leu	Val	Thr	Thr
								340		345			350		
Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys	Arg	Val	Lys	His
							355		360			365			
Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met	Ala	Thr	Phe
								370		375			380		
Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile	Leu	Ser	Arg
							385		390			395			400
Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile	Trp	Thr	Gly	Asp
								405		410			415		
Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln	Leu	Val	Leu
								420		425			430		
Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys	Asp	Ile	Gly	Gly
								435		440			445		
Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser	Met	Asp	Leu	Leu
								450		455			460		
Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe	Tyr	Arg	Ser	His
								465		470			475		
Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu	Pro	Asp	Tyr
								485		490			495		
Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg	Tyr	Lys	Phe	Leu
								500		505			510		
Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys	Gly	His	Pro
								515		520			525		
Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp	Asp	Asp	Met	Tyr
								530		535			540		
Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu	Leu	Tyr	Ala	Pro
								545		550			555		
Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro	Arg	Gly	Lys
								565		570			575		
Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly	Lys	Ser	Val	Val
								580		585			590		
Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu	Gly	Ser	Ile	Ile
								595		600			605		
Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu	Thr	Ser	Phe	Lys
								610		615			620		
Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Asn	Glu	Ile	Lys	Phe	
								625		630			635		
Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser	Glu	Lys	Pro
								645		650			655		
Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln	Val	Glu	Lys
								660		665			670		
Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys	Ile	Arg	Gly
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Lys	Ile	Asn	Leu	Glu											
								690							

<210> 6
<211> 2082
<212> DNA
<213> *Sulfolobus solfataricus*

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<400> 6

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aaggagcaca	tcatcggct	cggcgagaag	gccttcgagc	tggaccgcaa	gcgcaagcgc	240
tacgtgatgt	acaacgtgga	cgccggcgcc	tacaagaagt	accaggaccc	gctctacgtg	300
tccatccgc	tcttcatctc	cgtgaaggac	ggcgtggcca	ccggctactt	cttcaactcc	360
gcctccaagg	tgatcttgcg	cgtggcctc	gaggagtagc	acaagggtat	cgtgaccatc	420
ccggaggact	ccgtggagtt	ctacgtgatc	gagggcccg	gcatcgagga	cgtgctcgag	480
aagtacaccg	agctgaccgg	caagccgttc	ctcccggcga	tgtggccctt	cggctacatg	540
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tggtggccg	gcctcatctc	cgagtggctc	tcccaggcg	tggacggcat	ctggctcgac	960
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ccgggtcagt	tccgcgacga	ccgcctcg	accaccttcc	cgacaaacgt	gtgcactac	1080
ctccgcggca	agcgcgtgaa	gcacgagaag	gtgcgcaacg	cctaccgct	ctacgaggcg	1140
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aaggccaccc	acggcatcg	caccgagcc	gtgttcc	cgactacta	caaggagaag	1500
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tacctccgcg	agggtccat	catcccgtc	gagggcgac	agctgatcg	gtacggcgag	1860
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atcggttcca	actccaagga	gatccaggt	gagaagacca	tgcagaacac	ctacgtggcc	2040
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<211> 1818

<212> DNA

<213> Artificial Sequence

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<223> synthetic

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<211> 606

<212> PRT

<213> Artificial Sequence

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<223> synthetic

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Arg	Gly	Ala	Arg	Ala	Ser	Ala	Ala	Asp	Thr	Leu	Ser	Met	Arg	Thr	
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Ser	Ala	Arg	Ala	Ala	Pro	Arg	His	Gln	His	Gln	Gln	Ala	Arg	Arg	Gly
							50				55			60	
Ala	Arg	Phe	Pro	Ser	Leu	Val	Val	Cys	Ala	Ser	Ala	Gly	Met	Asn	Val
							65				70			75	80
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							85				90			95	
Gly	Asp	Val	Leu	Gly	Gly	Leu	Pro	Pro	Ala	Met	Ala	Ala	Asn	Gly	His
							100				105			110	
Arg	Val	Met	Val	Val	Ser	Pro	Arg	Tyr	Asp	Gln	Tyr	Lys	Asp	Ala	Trp
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Asp	Thr	Ser	Val	Val	Ser	Glu	Ile	Lys	Met	Gly	Asp	Gly	Tyr	Glu	Thr
							130				135			140	
Val	Arg	Phe	Phe	His	Cys	Tyr	Lys	Arg	Gly	Val	Asp	Arg	Val	Phe	Val
							145				150			155	160
Asp	His	Pro	Leu	Phe	Leu	Glu	Arg	Val	Trp	Gly	Lys	Thr	Glu	Glu	Lys
							165				170			175	
Ile	Tyr	Gly	Pro	Val	Ala	Gly	Thr	Asp	Tyr	Arg	Asp	Asn	Gln	Leu	Arg
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Phe	Ser	Leu	Leu	Cys	Gln	Ala	Ala	Leu	Glu	Ala	Pro	Arg	Ile	Leu	Ser
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Leu	Asn	Asn	Asn	Pro	Tyr	Phe	Ser	Gly	Pro	Tyr	Gly	Glu	Asp	Val	Val
							210				215			220	
Phe	Val	Cys	Asn	Asp	Trp	His	Thr	Gly	Pro	Leu	Ser	Cys	Tyr	Leu	Lys
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Ser	Asn	Tyr	Gln	Ser	His	Gly	Ile	Tyr	Arg	Asp	Ala	Lys	Thr	Ala	Phe
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Cys	Ile	His	Asn	Ile	Ser	Tyr	Gln	Gly	Arg	Phe	Ala	Phe	Ser	Asp	Tyr
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Asp	Gly	Tyr	Glu	Lys	Pro	Val	Glu	Gly	Arg	Lys	Ile	Asn	Trp	Met	Lys
							290				295			300	
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305 Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn
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<213> Artificial Sequence

<220>

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<211> 741

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

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					35			40			45				
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					50			55			60				
Pro	Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val
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Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr
					85			90			95				
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					100			105			110				
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Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr
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					180			185			190				
Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val
					195			200			205				
Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr
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275 280 285
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Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305 310 315 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
325 330 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
340 345 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
355 360 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
370 375 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385 390 395 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
405 410 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
420 425 430
Cys Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val
435 440 445
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450 455 460
Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly
465 470 475 480
Ile Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys
485 490 495
Tyr Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala
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Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg
515 520 525
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530 535 540
Pro Asp Val Met Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu
545 550 555 560
Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg
565 570 575
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580 585 590
Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp
595 600 605
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Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly
625 630 635 640
Leu Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg
645 650 655
Leu Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val
660 665 670
Ala Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr
675 680 685
Glu Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly
690 695 700
Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly
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<212> DNA
<213> Zea mays

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<210> 12
<211> 673
<212> DNA
<213> Zea mays

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<210> 13
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

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35 40 45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
50 55 60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65 70 75 80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
85 90 95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100 105 110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115 120 125
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130 135 140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145 150 155 160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165 170 175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180 185 190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195 200 205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
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Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225 230 235 240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245 250 255
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260 265 270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275 280 285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290 295 300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305 310 315 320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325 330 335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340 345 350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
355 360 365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
370 375 380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385 390 395 400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
405 410 415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
420 425 430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
435 440 445
Ser Tyr Cys Gly Val Gly
450

<210> 14

<211> 460

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 14

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
 20 25 30
 Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35 40 45
 Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50 55 60
 Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65 70 75 80
 Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85 90 95
 Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
 100 105 110
 Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
 115 120 125
 Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
 130 135 140
 Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
 145 150 155 160
 Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
 165 170 175
 Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
 180 185 190
 Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
 195 200 205
 Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
 210 215 220
 Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
 225 230 235 240
 Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
 245 250 255
 Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
 260 265 270
 Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
 275 280 285
 Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
 290 295 300
 Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
 305 310 315 320
 Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
 325 330 335
 Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
 340 345 350
 Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400
 Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 15

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 15

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
 1 5 10 15
 Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20 25 30
 Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45
 Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
 50 55 60
 Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
 65 70 75 80
 Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met Gln Ala Phe
 85 90 95
 Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
 100 105 110
 Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
 115 120 125
 Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
 130 135 140
 Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
 145 150 155 160
 Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
 165 170 175
 His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
 180 185 190
 Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
 195 200 205
 Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
 210 215 220
 Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
 225 230 235 240
 Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
 245 250 255
 Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile
 260 265 270
 Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
 275 280 285
 Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
 290 295 300
 Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
 305 310 315 320
 Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
 325 330 335
 Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
 340 345 350
 Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
 355 360 365
 Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
 370 375 380
 Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
 385 390 395 400

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His	Asp	Asn	Leu
405									410						415
Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp	Glu	Met	Ile
420								425						430	
Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr	Ile
435							440					445			
Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys	Phe
450						455				460					
Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp	Val
465						470			475					480	
Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro	Ala
								485		490				495	
Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr	Cys
						500		505						510	
Gly	Val	Gly	Thr	Ser	Ile										
					515										

<210> 16

<211> 820

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 16

Met	Leu	Ala	Ala	Leu	Ala	Thr	Ser	Gln	Leu	Val	Ala	Thr	Arg	Ala	Gly
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Leu	Gly	Val	Pro	Asp	Ala	Ser	Thr	Phe	Arg	Arg	Gly	Ala	Ala	Gln	Gly
								20	25					30	
Leu	Arg	Gly	Ala	Arg	Ala	Ser	Ala	Ala	Ala	Asp	Thr	Leu	Ser	Met	Arg
								35	40				45		
Thr	Ser	Ala	Arg	Ala	Ala	Pro	Arg	His	Gln	His	Gln	Gln	Ala	Arg	Arg
								50	55		60				
Gly	Ala	Arg	Phe	Pro	Ser	Leu	Val	Val	Cys	Ala	Ser	Ala	Gly	Ala	Met
								65	70		75		80		
Ala	Lys	Tyr	Leu	Glu	Leu	Glu	Gly	Gly	Val	Ile	Met	Gln	Ala	Phe	
								85	90		95				
Tyr	Trp	Asp	Val	Pro	Ser	Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Arg	Gln
								100	105				110		
Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro
								115	120				125		
Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro
								130	135		140				
Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu
								145	150		155		160		
Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr	Ala
								165	170		175				
His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg
								180	185		190				
Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp	Tyr	Thr	Trp
								195	200		205				
Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu
								210	215		220				
Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe	Gly
								225	230		235		240		
Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu
								245	250				255		
Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile
								260	265				270		
Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val	Val
								275	280				285		

60110USPCT1 Corrected SEQ LIST 2-2007.txt
Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
290 295 300
Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
305 310 315 320
Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
325 330 335
Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
340 345 350
Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
355 360 365
Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
370 375 380
Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
385 390 395 400
Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu
405 410 415
Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile
420 425 430
Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile
435 440 445
Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe
450 455 460
Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val
465 470 475 480
Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala
485 490 495
Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys
500 505 510
Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val Leu
515 520 525
Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg
530 535 540
Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly Ile
545 550 555 560
Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys Tyr
565 570 575
Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala Leu
580 585 590
Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg Asn
595 600 605
Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro
610 615 620
Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu Asp
625 630 635 640
Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Phe Glu Arg Met
645 650 655
Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val Val
660 665 670
Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp Val
675 680 685
Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln
690 695 700
Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu
705 710 715 720
Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu
725 730 735
Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala
740 745 750
Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu
755 760 765
Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly Pro
770 775 780
Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly

60110USPCT1 Corrected SEQ LIST 2-2007.txt
790 795 800
Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn
810 815

<210> 17
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 17
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15
Ala Thr Ser

<210> 18
 <211> 444
 <212> PRT
 <213> Thermotoga maritima

<400> 18
 Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys
 1 5 10 15
 Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val
 20 25 30
 Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe
 35 40 45
 Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr
 50 55 60
 Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe
 65 70 75 80
 Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu
 85 90 95
 Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu
 100 105 110
 Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu
 115 120 125
 Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu
 130 135 140
 Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala
 145 150 155 160
 Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile
 165 170 175
 Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu
 180 185 190
 Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Leu Glu Leu Glu Asn
 195 200 205
 Leu Ala Arg Phe Leu Arg Met Ala Val Glu Tyr Ala Lys Lys Ile Gly
 210 215 220
 Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys
 225 230 235 240
 His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Asn
 245 250 255
 His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala
 260 265 270
 Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile
 275 280 285

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu	Leu	Leu
290				295						300					
Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp	Thr	Thr	Leu
305				310					315					320	
Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys	Gly	Gly	Leu
				325				330				335			
Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	Glu	Asp	Leu
				340				345				350			
Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu	Gly	Phe	Lys
				355			360				365				
Ile	Ala	Tyr	Lys	Leu	Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys	Phe	Ile	Glu
				370			375				380				
Glu	Lys	Tyr	Arg	Ser	Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu	Ile	Val	Glu
				385			390			395			400		
Gly	Lys	Thr	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp	Lys	Glu
				405				410				415			
Asp	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	Ser	Leu	Leu
				420				425				430			
Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Ala	Glu	Leu	Arg				
				435				440							

<210> 19

<211> 1335

<212> DNA

<213> Thermotoga maritima

<400> 19

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cacctaagt	tctccgtggc	cttctggcac	accttcgtga	acgagggccg	cgaccgcTTc	180
ggcaccgcg	ccgcccggcg	cccgtggAAC	cgcttctccg	acccgatggA	caaggccTTC	240
gcccgggtgg	acgccccttt	cgagttctgc	gagaagctca	acatcgagta	tttctgtttc	300
cacgaccgcg	acatcgcccc	ggagggcaag	accctccgcg	agaccaacaa	gatcctcgac	360
aaggtgggtgg	agcgcatcaa	ggagcgcattg	aaggactcca	acgtgaagct	cctctggggc	420
accgccaacc	tcttctccca	cccgcgttac	atgcacggcg	ccgcccaccac	ctgctccgCC	480
gacgtgtttcg	cctacgcccgc	cgcccagggt	aagaaggccc	tggagatcac	caaggagctg	540
ggcggcgagg	gctacgtgtt	ctggggcgGC	cgcgagggt	acgagaccct	cctcaacacc	600
gacctcggcc	tggagctggA	gaacctcgcc	cgcttctcc	gcatggccgt	ggagtacGCC	660
aagaagatcg	gcttcacccgg	ccagttccTC	atcgagccGA	agccgaagga	gccgaccaAG	720
caccagtacg	acttcgacgt	ggccaccgcC	tacgccttcc	tcaagaacca	cgccctcgac	780
gagtacttca	agttcaacat	cgaggccAAc	cacGCCACCC	tcgcccggCCA	caccttccAG	840
cacgagctgc	gcatggcccG	catcctcgGC	aagctcggt	ccatcgacgc	caaccaggGC	900
gaccccttcc	tggctggga	caccgaccAG	ttcccgacca	acatctacga	caccaccCTC	960
gccatgtacg	aggtgatcaa	ggccggcgGC	ttcaccaagg	gccccctcaa	tttcgacGCC	1020
aaggtgcGCC	gcccctccta	caaggtggag	gacctttca	tcggccacat	cgccggcatg	1080
gacaccttCG	ccctcggctt	caagatcgCC	tacaagctcg	ccaaggacgg	cgtgttcgac	1140
aagttcatcg	aggagaagta	ccgctccTTc	aaggaggGC	tcggcaagga	gatcgtggag	1200
ggcaagacccg	acttcgagaa	gctggaggAG	tacatcatcg	acaaggagga	catcgagctg	1260
ccgtccggca	agcaggagta	cctggagtcc	ctcctcaact	cctacatcgT	gaagaccatc	1320
gccgagctgc	gctga					1335

<210> 20

<211> 444

<212> PRT

<213> Thermotoga neapolitana

<400> 20

Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Val	Gln	Phe	Glu	Gly	Lys
1				5				10			15				
Glu	Ser	Thr	Asn	Pro	Leu	Ala	Phe	Lys	Phe	Tyr	Asp	Pro	Glu	Glu	Ile
					20			25			30				
Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser	Val	Ala	Phe

60110USPCT1 Corrected SEQ LIST 2-2007.txt

35	40	45	
Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr			
50	55	60	
Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe			
65	70	75	80
Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu			
85	90	95	
Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu			
100	105	110	
Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu			
115	120	125	
Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu			
130	135	140	
Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala			
145	150	155	160
Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile			
165	170	175	
Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu			
180	185	190	
Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn			
195	200	205	
Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly			
210	215	220	
Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys			
225	230	235	240
His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser			
245	250	255	
His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala			
260	265	270	
Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile			
275	280	285	
Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu			
290	295	300	
Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu			
305	310	315	320
Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly Leu			
325	330	335	
Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu			
340	345	350	
Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys			
355	360	365	
Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu			
370	375	380	
Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu			
385	390	395	400
Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu			
405	410	415	
Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile			
420	425	430	
Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg			
435	440		

<210> 21

<211> 1335

<212> DNA

<213> Thermotoga neapolitana

<400> 21

atggccgagt tcttccccga gatcccgaag gtgcagttcg agggcaagga gtccaccaac 60
 ccgctcgctt tcaagttcta cgacccggag gagatcatcg acggcaagcc gctcaaggac 120
 cacctaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgaccggttc 180
 ggcgacccga ccgcccggaccg cccgtggAAC cgctacaccg acccgatggA caaggccttc 240

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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gcccgcgtgg acgccctttt cgagttctgc gagaagctca acatcgagta cttctgcttc 300
cacgaccgcg acatcgcccc ggagggcaag accctccgcg agaccaacaa gatcctcgac 360
aagggttgtt agcgcatcaa ggagcgcatt aaggactcca acgtgaagct cctctggggc 420
accgc当地 acc tcttctccca cccgc当地 tac atgc当地 cggcg cgc当地 accac ctgctccgc 480
gacgtgttcg cctacgc当地 cggcc当地 agggtg aagaaggccc tggagatcac caaggagctg 540
ggc当地 cggagg gctacgtgtt ctggggc当地 cgc当地 agggtc acgagaccct cctcaacacc 600
gacctcggtt tcgagctgga gaacctcgcc cgcttccctt gcatggccgt ggactacgcc 660
aagcgc当地 cg gcttccaccgg ccagttccctc atcgagccga agccgaagga gccgaccaag 720
caccagtc当地 ctgc当地 acgttccctc tcaagttccca cggc当地 ctgc当地 780
gagtacttca agttcaacat cgaggccaa cacgccc当地 tcgccc当地 caccttccag 840
cagc当地 gctg gcatggcccg catcctcgcc aagctcggtt ccatcgacgc caaccaggc 900
gacctccctt tcggctggga caccgaccag ttcccgacca acgtgtacga caccaccctc 960
gccatgtacg aggtgatcaa ggccggc当地 ttc当地 accaagg gc当地 ggccctcaa cttcgacgcc 1020
aagggtgc当地 gccc当地 ctta caaggtggag gaccttccat tcggccacat cgccggcatg 1080
gacaccttc当地 cc当地 ctccgtt caaggtggcc tacaagctcg tgaaggacgg cgtgctcgac 1140
aagttcatcg aggagaagta cc当地 ctccctt cgc当地 agggtc tcgccc当地 cga catcgtggag 1200
ggcaagggtgg acttc当地 gagaa gctggaggag tacatcatcg acaaggagac catcgagctg 1260
ccgtccggca agcaggagta cctggagttcc ctc当地 catcaact cctacatcgta gaagaccatc 1320
ctggagctgc gctga 1335

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<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 22
agcgaattca tggcggctct ggccacgt 28

<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 23
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<210> 24
<211> 825
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 24
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1 5 10 15
Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
20 25 30
Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
35 40 45
Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
50 55 60
Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
65 70 75 80
Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
85 90 95

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Asp	Thr	Ser	Pro	Arg	Ile	Phe	Phe	Ala	Gln	Ala	Arg	Ser	Asn	Lys	Val
			100					105						110	
Ile	Glu	Ala	Phe	Leu	Thr	Asn	Pro	Val	Asp	Thr	Lys	Lys	Lys	Glu	Leu
	115						120				125				
Phe	Lys	Val	Thr	Val	Asp	Gly	Lys	Glu	Ile	Pro	Val	Ser	Arg	Val	Glu
	130					135				140					
Lys	Ala	Asp	Pro	Thr	Asp	Ile	Asp	Val	Thr	Asn	Tyr	Val	Arg	Ile	Val
	145						150			155				160	
Leu	Ser	Glu	Ser	Leu	Lys	Glu	Glu	Asp	Leu	Arg	Lys	Asp	Val	Glu	Leu
					165				170				175		
Ile	Ile	Glu	Gly	Tyr	Lys	Pro	Ala	Arg	Val	Ile	Met	Met	Glu	Ile	Leu
				180					185				190		
Asp	Asp	Tyr	Tyr	Tyr	Asp	Gly	Glu	Leu	Gly	Ala	Val	Tyr	Ser	Pro	Glu
		195					200					205			
Lys	Thr	Ile	Phe	Arg	Val	Trp	Ser	Pro	Val	Ser	Lys	Trp	Val	Lys	Val
	210					215					220				
Leu	Leu	Phe	Lys	Asn	Gly	Glu	Asp	Thr	Glu	Pro	Tyr	Gln	Val	Val	Asn
	225					230				235				240	
Met	Glu	Tyr	Lys	Gly	Asn	Gly	Val	Trp	Glu	Ala	Val	Val	Glu	Gly	Asp
					245				250				255		
Leu	Asp	Gly	Val	Phe	Tyr	Leu	Tyr	Gln	Leu	Glu	Asn	Tyr	Gly	Lys	Ile
			260					265				270			
Arg	Thr	Thr	Val	Asp	Pro	Tyr	Ser	Lys	Ala	Val	Tyr	Ala	Asn	Asn	Gln
		275				280					285				
Glu	Ser	Ala	Val	Val	Asn	Leu	Ala	Arg	Thr	Asn	Pro	Glu	Gly	Trp	Glu
					295					300					
Asn	Asp	Arg	Gly	Pro	Lys	Ile	Glu	Gly	Tyr	Glu	Asp	Ala	Ile	Ile	Tyr
		305				310				315				320	
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val	Lys
						325				330			335		
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala	Pro
			340					345				350			
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val	Thr
		355				360					365				
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu	Leu
		370				375				380					
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr	Leu
		385				390				395				400	
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro	His
						405				410			415		
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His
						420				425			430		
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly	Ile
		435					440				445				
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr	Arg
		450					455				460				
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn	Val
		465				470				475				480	
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr	Val
						485				490			495		
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln
				500				505				510			
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu
						515				520			525		
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly	Gly
		530				535				540					
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr	His
		545				550				555				560	
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser	Val
						565				570			575		
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys	Glu
				580				585				590			
Thr	Lys	Ile	Lys	Arg	Gly	Val	Val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly	Lys

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595	600	605
Leu Ile Lys Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala		
610	615	620
Ala Cys His Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala		
625	630	635
Lys Ala Asp Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala		640
645	650	655
Gln Lys Leu Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe		
660	665	670
Leu His Gly Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn		
675	680	685
Ser Tyr Asn Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys		
690	695	700
Leu Gln Phe Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu		
705	710	715
Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys		
725	730	735
Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met		
740	745	750
Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile		
755	760	765
Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys		
770	775	780
Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu		
785	790	795
Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu		800
805	810	815
Tyr Arg Glu Ser Glu Lys Asp Glu Leu		
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<210> 25

<211> 2478

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 25

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gtggccgtgg tgaagctccc gatggacctc accaagggtgg gcatcatcg ggcgcctcaac	180
gagtggcagg cgaaggacgt ggccaaggac cgcttcatcg agatcaagga cggcaaggcc	240
gaggtgtgga tactccaggg cgtggaggag atcttctacg agaagccgga cacctccccg	300
cgcattttct tcgcccaggc ccgctccaac aaggtatcg aggccctcct cacaacccg	360
gtggacaccca agaagaagga gctgttcaag gtgaccgtcg acggcaagga gatcccggtg	420
tcccgctgtgg agaaggccga cccgaccgac atcgacgtga ccaactacgt gcgcatcg	480
ctctcccgagt ccctcaagga ggaggacctc cgcaaggacg tggagctgat catcgaggc	540
tacaaggccgg cccgcgtgat catgatggag atcctcgacg actactacta cgacggcgag	600
ctggggggcgg tgtactcccc ggagaagacc atcttcccgcg tgtggtcccc ggtgtccaag	660
tgggtgaagg tgctcctt caagaacccg gaggacaccg agccgtacca ggtggtaac	720
atggagtaca agggcaacgg cgtgtggag gccgtggtg agggcgacct cgacggcg	780
ttctacctct accagctgga gaactacccg aagatccgca ccaccgtgga cccgtactcc	840
aaggccgtgt acgccaacaa ccaggagtct gcagtggta acctcgcccg cacaacccg	900
gagggctgg agaacgaccg cggcccgaag atcgagggtc acgaggacgc catcatctac	960
gagatccaca tcgcccacat caccggctg gagaactccg gcgtgaagaa caaggccctc	1020
tacccctggcc tcaccggagga gaacaccaag gccccggcg gcgtgaccac cggcctctcc	1080
cacccctcggtt agctggcggt gacccacgtc cacatcctcc cgttcttcga ttctacacc	1140
ggcgcacgac tggacaagga cttcgagaag tactacaact ggggctacga cccgtacctc	1200
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gaggtgaagg agatggtgaa ggccctccac aagcacggca tcggcgtgat catggacatg	1320
gtgttcccgcc acacctacgg catcgccgag ctgtccgcct tcgaccagac cgtgccgtac	1380

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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aaggagtacc acatcgacgg cttccgcttc gaccagatgg gcctcatcga caagaagacc 1560
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ccgtggggcg gctggggggc cccgatccgc ttccggcaagt ccgacgtggc cggcacccac 1680
gtggccgcct tcaacgcacg gtccgcgc gccatccgcg gctccgtgtt caaccgtcc 1740
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ggctccatca actacgcacgg caagctcatc aagtccctcg ccctcgaccc ggaggagacc 1860
atcaactacg cgcctgcca cgacaaccac accctctggg acaagaacta cctcgccgccc 1920
aaggccgaca agaagaagga gtggaccggag gaggagctga agaacgcccga gaagctcgcc 1980
ggccgcattcc tcctcaactag tcagggcggtg ccgttccctcc acggcgccca ggacttctgc 2040
cgaccacca acttcaacga caactcctac aacgccccga tctccatcaa cggcttcgac 2100
tacgagcgcgca agtcccgat catcgacgtg ttcaactacc acaagggcct catcaagctc 2160
cgcaaggagg acccggccctt ccgcctcaag aacgcccggag agatcaagaa gcacctggag 2220
ttcctcccg gccccgcgcg catcggtgcc ttcatgctca aggaccacgc cggcggcgac 2280
ccgtggagg acatcggtt gatctacaac ggcaacctgg agaagaccac ctacaagctc 2340
ccggagggca agtggAACGT ggtggtaaac tcccagaagg ccggcaccga ggtgatcgag 2400
accgtggagg gcaccatcga gctggaccccg ctctccgcct acgtgctcta cgcgagtc 2460
gagaaggacg agctgtga 2478
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<210> 26

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 26

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Ala	Ser		
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Ala	Thr	Ser	Met	Glu	Thr	Ile	Lys	Ile	Tyr	Glu	Asn	Lys	Gly	Val	Tyr
			20			25					30				
Lys	Val	Val	Ile	Gly	Glu	Pro	Phe	Pro	Pro	Ile	Glu	Phe	Pro	Leu	Glu
			35			40				45					
Gln	Lys	Ile	Ser	Ser	Asn	Lys	Ser	Leu	Ser	Glu	Leu	Gly	Leu	Thr	Ile
	50					55				60					
val	Gln	Gln	Gly	Asn	Lys	Val	Ile	Val	Glu	Lys	Ser	Leu	Asp	Leu	Lys
	65					70			75			80			
Glu	His	Ile	Ile	Gly	Leu	Gly	Glu	Lys	Ala	Phe	Glu	Leu	Asp	Arg	Lys
			85				90				95				
Arg	Lys	Arg	Tyr	Val	Met	Tyr	Asn	Val	Asp	Ala	Gly	Ala	Tyr	Lys	Lys
			100			105			110						
Tyr	Gln	Asp	Pro	Leu	Tyr	val	Ser	Ile	Pro	Leu	Phe	Ile	Ser	Val	Lys
		115				120			125						
Asp	Gly	Val	Ala	Thr	Gly	Tyr	Phe	Phe	Asn	Ser	Ala	Ser	Lys	Val	Ile
	130				135				140						
Phe	Asp	Val	Gly	Leu	Glu	Glu	Tyr	Asp	Lys	Val	Ile	Val	Thr	Ile	Pro
	145				150				155			160			
Glu	Asp	Ser	Val	Glu	Phe	Tyr	Val	Ile	Glu	Gly	Pro	Arg	Ile	Glu	Asp
				165				170			175				
Val	Leu	Glu	Lys	Tyr	Thr	Glu	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Pro	Pro
			180			185			190						
Met	Trp	Ala	Phe	Gly	Tyr	Met	Ile	Ser	Arg	Tyr	Ser	Tyr	Tyr	Pro	Gln
			195			200			205						
Asp	Lys	Val	Val	Glu	Leu	Val	Asp	Ile	Met	Gln	Lys	Glu	Gly	Phe	Arg
		210			215			220							
Val	Ala	Gly	Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu
	225			230				235		240					
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile	Asp
			245			250			255						
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly
	260					265			270						

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly	Lys
275						280						285			
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp	Pro
290						295					300				
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp
305						310				315					320
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile
						325				330			335		
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu	Ile
						340				345			350		
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg	Leu
						355				360			365		
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys	Arg
						370				375			380		
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met
						385				390			395		400
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile
						405				410			415		
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile	Trp
						420				425			430		
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln
						435				440			445		
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys	Asp
						450				455			460		
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser	Met
						465				470			475		480
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe	Tyr
						485				490			495		
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu
						500				505			510		
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	val	Glu	Leu	Arg	Tyr
						515				520			525		
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys
						530				535			540		
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp	Asp
						545				550			555		560
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu	Leu
						565				570			575		
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro
						580				585			590		
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly	Lys
						595				600			605		
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu	Gly
						610				615			620		
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu	Thr
						625				630			635		640
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn	Glu
						645				650			655		
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser
						660				665			670		
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln
						675				680			685		
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys
						690				695			700		
Ile	Arg	Gly	Lys	Ile	Asn	Leu	Glu	Ser	Glu	Lys	Asp	Glu	Leu		
						705				710			715		

<210> 27
<211> 712
<212> PRT
<213> Artificial Sequence

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<223> synthetic

<400> 27

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Ala Ser
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 Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
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 Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
 35 40 45
 Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
 50 55 60
 Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
 65 70 75 80
 Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
 85 90 95
 Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
 100 105 110
 Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
 115 120 125
 Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
 130 135 140
 Phe Asp Val Gly Leu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
 145 150 155 160
 Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
 165 170 175
 Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
 180 185 190
 Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
 195 200 205
 Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
 210 215 220
 Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu
 225 230 235 240
 Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
 245 250 255
 Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
 260 265 270
 Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
 275 280 285
 Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
 290 295 300
 Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
 305 310 315 320
 Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
 325 330 335
 Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
 340 345 350
 Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu
 355 360 365
 Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
 370 375 380
 Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
 385 390 395 400
 Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
 405 410 415
 Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
 420 425 430
 Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
 435 440 445
 Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
 450 455 460
 Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met

60110USPCT1 Corrected SEQ LIST 2-2007.txt

465	470	475	480												
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe	Tyr
				485		490									495
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu
				500		505									510
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	val	Glu	Leu	Arg	Tyr
				515		520									525
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys
				530		535									540
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp	Asp
				545		550									560
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu	Leu
				565		570									575
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro
				580		585									590
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly	Lys
				595		600									605
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu	Gly
				610		615									620
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu	Thr
				625		630									640
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn	Glu
				645		650									655
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser
				660		665									670
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln
				675		680									685
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys
				690		695									700
Ile	Arg	Gly	Lys	Ile	Asn	Leu	Glu								
				705		710									

<210> 28

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 28

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ala	Ser	
1			5				10							15	
Ala	Thr	Ser	Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Ile	Gln	Phe
				20			25								30
Glu	Gly	Lys	Glu	Ser	Thr	Asn	Pro	Leu	Ala	Phe	Arg	Phe	Tyr	Asp	Pro
				35		40									45
Asn	Glu	Val	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser
				50		55									60
Val	Ala	Phe	Trp	His	Thr	Phe	Val	Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly
				65		70									80
Asp	Pro	Thr	Ala	Glu	Arg	Pro	Trp	Asn	Arg	Phe	Ser	Asp	Pro	Met	Asp
				85			90								95
Lys	Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu
				100			105								110
Asn	Ile	Glu	Tyr	Phe	Cys	Phe	His	Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly
				115			120								125
Lys	Thr	Leu	Arg	Glu	Thr	Asn	Lys	Ile	Leu	Asp	Lys	Val	Val	Glu	Arg
				130			135								140
Ile	Lys	Glu	Arg	Met	Lys	Asp	Ser	Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr
				145			150								160
Ala	Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr

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Cys	Ser	Ala	Asp	165	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala
				180				170					175			
Leu	Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly	
				195				185				190				
Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Leu	Glu	
				210				200			205					
Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Glu	Tyr	Ala	Lys	
				225				230			235			240		
Lys	Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu	
				245				250			255					
Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe	
				260				265			270					
Leu	Lys	Asn	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala	
				275				280			285					
Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met	
				290				295			300					
Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	
				305				310			315			320		
Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp	
				325				330			335					
Thr	Thr	Leu	Ala	Met	Tyr	Glu	val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys	
				340				345			350					
Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	
				355				360			365					
Glu	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu	
				370				375			380					
Gly	Phe	Lys	Ile	Ala	Tyr	Lys	Leu	Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys	
				385				390			395			400		
Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu	
				405				410			415					
Ile	Val	Glu	Gly	Lys	Thr	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	
				420				425			430					
Asp	Lys	Glu	Asp	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	
				435				440			445					
Ser	Leu	Leu	Asn	Ser	Tyr	Ile	val	Lys	Thr	Ile	Ala	Glu	Leu	Arg	Ser	
				450				455			460					
Glu	Lys	Asp	Glu	Leu												
				465												

<210> 29

<211> 469

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic

<400> 29

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Ala	Ser		
1			5				10				15				
Ala	Thr	Ser	Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Val	Gln	Phe
							20			25			30		
Glu	Gly	Lys	Glu	Ser	Thr	Asn	Pro	Leu	Ala	Phe	Lys	Phe	Tyr	Asp	Pro
							35			40			45		
Glu	Glu	Ile	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser
							50			55			60		
val	Ala	Phe	Trp	His	Thr	Phe	Val	Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly
				65			70			75			80		
Asp	Pro	Thr	Ala	Asp	Arg	Pro	Trp	Asn	Arg	Tyr	Thr	Asp	Pro	Met	Asp
							85			90			95		
Lys	Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu

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Asn	Ile	Glu	Tyr	Phe	Cys	Phe	His	Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly
100							105					110			
115							115	120				125			
Lys	Thr	Leu	Arg	Glu	Thr	Asn	Lys	Ile	Leu	Asp	Lys	Val	Val	Glu	Arg
130							130	135				140			
Ile	Lys	Glu	Arg	Met	Lys	Asp	Ser	Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr
145							145	150				155			160
Ala	Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr
							165		170			175			
Cys	Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala
							180		185			190			
Leu	Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly
							195		200			205			
Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Phe	Glu
							210		215			220			
Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Asp	Tyr	Ala	Lys
							225		230			235			240
Arg	Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu
							245		250			255			
Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe
							260		265			270			
Leu	Lys	Ser	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala
							275		280			285			
Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met
							290		295			300			
Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp
							305		310			315			320
Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Val	Tyr	Asp
							325		330			335			
Thr	Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys
							340		345			350			
Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val
							355		360			365			
Glu	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu
							370		375			380			
Gly	Phe	Lys	Val	Ala	Tyr	Lys	Leu	Val	Lys	Asp	Gly	Val	Leu	Asp	Lys
							385		390			395			400
Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Arg	Glu	Gly	Ile	Gly	Arg	Asp
							405		410			415			
Ile	Val	Glu	Gly	Lys	Val	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile
							420		425			430			
Asp	Lys	Glu	Thr	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu
							435		440			445			
Ser	Leu	Ile	Asn	Ser	Tyr	Ile	val	Lys	Thr	Ile	Leu	Glu	Leu	Arg	Ser
							450		455			460			
Glu	Lys	Asp	Glu	Leu											
							465								

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 30

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ser
 1 5 10 15

Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30

Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro

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Glu	Glu	Ile	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser
35					40					45					
50					55					60					
val	Ala	Phe	Trp	His	Thr	Phe	Val	Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly
65					70				75					80	
Asp	Pro	Thr	Ala	Asp	Arg	Pro	Trp	Asn	Arg	Tyr	Thr	Asp	Pro	Met	Asp
					85				90					95	
Lys	Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu
					100			105					110		
Asn	Ile	Glu	Tyr	Phe	Cys	Phe	His	Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly
					115			120				125			
Lys	Thr	Leu	Arg	Glu	Thr	Asn	Lys	Ile	Leu	Asp	Lys	Val	Val	Glu	Arg
					130			135				140			
Ile	Lys	Glu	Arg	Met	Lys	Asp	Ser	Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr
					145			150			155			160	
Ala	Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr
					165			170					175		
Cys	Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Gln	Val	Lys	Lys	Ala	
					180			185				190			
Leu	Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly
					195			200				205			
Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Phe	Glu
					210			215				220			
Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Asp	Tyr	Ala	Lys
					225			230			235			240	
Arg	Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu
					245			250				255			
Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe
					260			265				270			
Leu	Lys	Ser	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala
					275			280				285			
Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met
					290			295				300			
Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp
					305			310			315			320	
Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Val	Tyr	Asp
					325			330				335			
Thr	Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys
					340			345				350			
Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val
					355			360				365			
Glu	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu
					370			375				380			
Gly	Phe	Lys	Val	Ala	Tyr	Lys	Leu	Val	Lys	Asp	Gly	Val	Leu	Asp	Lys
					385			390			395			400	
Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Arg	Glu	Gly	Ile	Gly	Arg	Asp
					405			410				415			
Ile	Val	Glu	Gly	Lys	Val	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile
					420			425				430			
Asp	Lys	Glu	Thr	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu
					435			440				445			
Ser	Leu	Ile	Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Leu	Glu	Leu	Arg	
					450			455				460			

<210> 31

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

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<400> 31
Met Gly Lys Asn Gly Asn Leu Cys Cys Phe Ser Leu Leu Leu Leu
1 5 10 15
Leu Ala Gly Leu Ala Ser Gly His Gln
20 25

<210> 32
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 32
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
1 5 10 15
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
20 25 30

<210> 33
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 33
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Ala Ser
1 5 10 15
Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
20 25 30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
35 40 45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
50 55 60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65 70 75 80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
85 90 95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100 105 110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115 120 125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130 135 140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145 150 155 160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165 170 175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180 185 190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195 200 205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210 215 220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225 230 235 240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245 250 255

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Ser	Gly	Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala
				260				265					270		
Ala	Phe	Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn
				275				280				285			
Gly	Gly	Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val
				290			295			300					
Ala	Asn	His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala
				305			310			315			320		
Phe	Ile	Leu	Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr
				325			330			335					
Glu	Glu	Trp	Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His
				340			345			350					
Asp	Asn	Leu	Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp
				355			360			365					
Glu	Met	Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile
				370			375			380					
Thr	Tyr	Ile	Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val
				385			390			395			400		
Pro	Lys	Phe	Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly
				405			410			415					
Gly	Trp	Val	Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu
				420			425			430					
Ala	Pro	Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp
				435			440			445					
Ser	Tyr	Cys	Gly	Val	Gly	Ser	Glu	Lys	Asp	Glu	Leu				
				450			455			460					

<210> 34

<211> 825

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 34

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Leu	Ala	Ser	
1			5				10				15				
Ala	Thr	Ser	Ala	Gly	His	Trp	Tyr	Lys	His	Gln	Arg	Ala	Tyr	Gln	Phe
					20		25			30					
Thr	Gly	Glu	Asp	Asp	Phe	Gly	Lys	Val	Ala	Val	Val	Lys	Leu	Pro	Met
					35		40			45					
Asp	Leu	Thr	Lys	Val	Gly	Ile	Ile	Val	Arg	Leu	Asn	Glu	Trp	Gln	Ala
					50		55			60					
Lys	Asp	Val	Ala	Lys	Asp	Arg	Phe	Ile	Glu	Ile	Lys	Asp	Gly	Lys	Ala
				65		70		75		80					
Glu	Val	Trp	Ile	Leu	Gln	Gly	Val	Glu	Glu	Ile	Phe	Glu	Lys	Pro	
					85		90			95					
Asp	Thr	Ser	Pro	Arg	Ile	Phe	Phe	Ala	Gln	Ala	Arg	Ser	Asn	Lys	Val
					100		105			110					
Ile	Glu	Ala	Phe	Leu	Thr	Asn	Pro	Val	Asp	Thr	Lys	Lys	Lys	Glu	Leu
					115		120			125					
Phe	Lys	Val	Thr	Val	Asp	Gly	Lys	Glu	Ile	Pro	Val	Ser	Arg	Val	Glu
					130		135			140					
Lys	Ala	Asp	Pro	Thr	Asp	Ile	Asp	Val	Thr	Asn	Tyr	Val	Arg	Ile	Val
				145		150		155		160					
Leu	Ser	Glu	Ser	Leu	Lys	Glu	Glu	Asp	Leu	Arg	Lys	Asp	Val	Glu	Leu
					165		170			175					
Ile	Ile	Glu	Gly	Tyr	Lys	Pro	Ala	Arg	Val	Ile	Met	Met	Glu	Ile	Leu
				180		185		190		195					
Asp	Asp	Tyr	Tyr	Tyr	Asp	Gly	Glu	Leu	Gly	Ala	Val	Tyr	Ser	Pro	Glu
				195		200			205						

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Lys	Thr	Ile	Phe	Arg	Val	Trp	Ser	Pro	Val	Ser	Lys	Trp	Val	Lys	Val
210					215						220				
Leu	Leu	Phe	Lys	Asn	Gly	Glu	Asp	Thr	Glu	Pro	Tyr	Gln	Val	Val	Asn
225					230				235						240
Met	Glu	Tyr	Lys	Gly	Asn	Gly	val	Trp	Glu	Ala	Val	Val	Glu	Gly	Asp
					245				250				255		
Leu	Asp	Gly	Val	Phe	Tyr	Leu	Tyr	Gln	Leu	Glu	Asn	Tyr	Gly	Lys	Ile
					260			265				270			
Arg	Thr	Thr	Val	Asp	Pro	Tyr	Ser	Lys	Ala	Val	Tyr	Ala	Asn	Asn	Gln
					275			280			285				
Glu	Ser	Ala	Val	Val	Asn	Leu	Ala	Arg	Thr	Asn	Pro	Glu	Gly	Trp	Glu
					290			295			300				
Asn	Asp	Arg	Gly	Pro	Lys	Ile	Glu	Gly	Tyr	Glu	Asp	Ala	Ile	Ile	Tyr
					305		310		315				320		
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val	Lys
					325			330				335			
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala	Pro
					340			345			350				
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val	Thr
					355			360			365				
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu	Leu
					370		375			380					
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr	Leu
					385		390		395				400		
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro	His
					405			410				415			
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His
					420			425				430			
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly	Ile
					435			440			445				
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr	Arg
					450		455		460						
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn	Val
					465		470		475				480		
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr	Val
					485			490				495			
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln
					500			505				510			
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu
					515			520				525			
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly	Gly
					530			535			540				
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr	His
					545		550		555				560		
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser	Val
					565			570				575			
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys	Glu
					580			585				590			
Thr	Lys	Ile	Lys	Arg	Gly	val	val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly	Lys
					595			600				605			
Leu	Ile	Lys	Ser	Phe	Ala	Leu	Asp	Pro	Glu	Glu	Thr	Ile	Asn	Tyr	Ala
					610			615			620				
Ala	Cys	His	Asp	Asn	His	Thr	Leu	Trp	Asp	Lys	Asn	Tyr	Leu	Ala	Ala
					625		630		635				640		
Lys	Ala	Asp	Lys	Lys	Lys	Glu	Trp	Thr	Glu	Glu	Leu	Lys	Asn	Ala	
					645			650				655			
Gln	Lys	Leu	Ala	Gly	Ala	Ile	Leu	Leu	Thr	Ser	Gln	Gly	val	Pro	Phe
					660			665				670			
Leu	His	Gly	Gly	Gln	Asp	Phe	Cys	Arg	Thr	Thr	Asn	Phe	Asn	Asp	Asn
					675			680				685			
Ser	Tyr	Asn	Ala	Pro	Ile	Ser	Ile	Asn	Gly	Phe	Asp	Tyr	Glu	Arg	Lys
					690			695			700				
Leu	Gln	Phe	Ile	Asp	Val	Phe	Asn	Tyr	His	Lys	Gly	Leu	Ile	Lys	Leu

60110USPCT1 Corrected SEQ LIST 2-2007.txt

705	Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys	710	715	720
	725	730	735	
Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met	740	745	750	
Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile	755	760	765	
Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys	770	775	780	
Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu	785	790	795	800
Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu	805	810	815	
Tyr Arg Glu Ser Glu Lys Asp Glu Leu	820	825		

<210> 35
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 35
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Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
20 25 30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
35 40 45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
50 55 60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65 70 75 80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
85 90 95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100 105 110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115 120 125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130 135 140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145 150 155 160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165 170 175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180 185 190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195 200 205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210 215 220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225 230 235 240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245 250 255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
260 265 270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275 280 285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val

60110USPCT1 Corrected SEQ LIST 2-2007.txt

290	295	300														
Ala	Asn	His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	
305																320
Phe	Ile	Leu	Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr	
																325
Glu	Glu	Trp	Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His	
																340
Asp	Asn	Leu	Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp	
																355
Glu	Met	Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	
																370
Thr	Tyr	Ile	Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val	
																385
Pro	Lys	Phe	Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	
																405
Gly	Trp	Trp	Val	Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu
																420
Ala	Pro	Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	
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Ser	Tyr	Cys	Gly	Val	Gly	Ser	Glu	Lys	Asp	Glu	Leu					450
																460

<210> 36

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 36

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																20
Lys	Val	Val	Ile	Gly	Glu	Pro	Phe	Pro	Pro	Ile	Glu	Phe	Pro	Leu	Glu	
																35
Gln	Lys	Ile	Ser	Ser	Asn	Lys	Ser	Leu	Ser	Glu	Leu	Gly	Leu	Thr	Ile	
																50
Val	Gln	Gln	Gly	Asn	Lys	Val	Ile	Val	Glu	Lys	Ser	Leu	Asp	Leu	Lys	
																65
Glu	His	Ile	Ile	Gly	Leu	Gly	Glu	Lys	Ala	Phe	Glu	Leu	Asp	Arg	Lys	
																85
Arg	Lys	Arg	Tyr	Val	Met	Tyr	Asn	Val	Asp	Ala	Gly	Ala	Tyr	Lys	Lys	
																100
Tyr	Gln	Asp	Pro	Leu	Tyr	Val	Ser	Ile	Pro	Leu	Phe	Ile	Ser	Val	Lys	
																115
Asp	Gly	Val	Ala	Thr	Gly	Tyr	Phe	Phe	Asn	Ser	Ala	Ser	Lys	Val	Ile	
																130
Phe	Asp	Val	Gly	Leu	Glu	Glu	Tyr	Asp	Lys	Val	Ile	Val	Thr	Ile	Pro	
																145
Glu	Asp	Ser	Val	Glu	Phe	Tyr	Val	Ile	Glu	Gly	Pro	Arg	Ile	Glu	Asp	
																165
Val	Leu	Glu	Lys	Tyr	Thr	Glu	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Pro	Pro	
																180
Met	Trp	Ala	Phe	Gly	Tyr	Met	Ile	Ser	Arg	Tyr	Ser	Tyr	Tyr	Pro	Gln	
																195
Asp	Lys	Val	Val	Glu	Leu	Val	Asp	Ile	Met	Gln	Lys	Glu	Gly	Phe	Arg	
																210
Val	Ala	Gly	Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu	
																225
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile	Asp	
																230

60110USPCT1 Corrected SEQ LIST 2-2007.txt

	245	250	255												
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly
			260		265									270	
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly	Lys
			275		280									285	
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp	Pro
			290		295								300		
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp
			305		310									320	
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile
			325											335	
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu	Ile
			340											350	
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg	Leu
			355											365	
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys	Arg
			370												
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met
			385											400	
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile
			405											415	
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile	Trp
			420											430	
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln
			435											445	
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys	Asp
			450											460	
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser	Met
			465											480	
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe	Tyr
			485											495	
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu
			500											510	
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg	Tyr
			515											525	
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys
			530											540	
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp	Asp
			545											560	
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu	Leu
			565											575	
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro
			580											590	
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly	Lys
			595											605	
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu	Gly
			610											620	
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu	Thr
			625											640	
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Asn	Glu	
			645											655	
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser
			660											670	
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln
			675											685	
val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys
			690											700	
Ile	Arg	Gly	Lys	Ile	Asn	Leu	Glu	Ser	Glu	Lys	Asp	Glu	Leu		
			705											715	

<210> 37
<211> 1434

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<212> DNA

<213> Thermotoga maritima

<400> 37

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 accctgggtgc cacgcgggttc catggccgag ttcttcccg agatcccgaa gatccagttc 120
 gagggcaagg agtccaccaa cccgctcgcc ttccgcttct acgaccgaa cgaggtgatc 180
 gacggcaagc cgctcaagga ccacactaag ttctccgtgg cttctggca caccttcgtg 240
 aacgagggcc gcgaccggtt cgccgaccgg accgcccggc gcccgtggaa ccgcttctcc 300
 gaccggatgg acaaggcctt cgcccggtg gacgcccctt tcgagttctg cgagaagctc 360
 aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggagggcaa gaccctccgc 420
 gagaccaaca agatcctcga caaggtggtg gagcgcatca aggagcgtt gaaggactcc 480
 aacgtgaagc tcctctgggg caccgccaac ctcttctccc acccgcgtt catgcacggc 540
 gcccacca cctgctccgc cgacgtgttc gcctacgccc ccgcccaggta gaagaaggcc 600
 ctggagatca ccaaggagct gggcggcgag ggctacgtgt tctggggcg ccgcgaggcc 660
 tacagaccc tcctcaacac cgacctcgcc ctggagctgg agaacctcgc ccgcttctcc 720
 cgcatggccg tggagtacgc caagaagatc ggcttcaccg gccagttcct catcgagccg 780
 aagccgaagg agccgaccaa gcaccagttt gacttcgacg tggccaccgc ctacgccttc 840
 ctcaagaacc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgcccacc 900
 ctcggccggcc acaccttcca gcacgagctg cgcatggccc gcacccctcgg caagctcggc 960
 tccatcgacg ccaaccaggcg cgaccccttc ctcggctggg acaccgacca gttcccgacc 1020
 aacatctacg acaccaccct cgccatgtac gaggtgatca aggccggcg ccgttcccaag 1080
 ggcggcctca acttcgacgc caaggtgcgc cgccctccct acaagggtgga ggacctcttc 1140
 atcggccaca tcgcccggcat ggacacccctt gcccctggct tcaagatcgc ctacaagctc 1200
 gccaaggacg gcgtgttcga caagttcatc gaggagaagt accgctcctt caaggaggcc 1260
 atcggcaagg agatcgtgga gggcaagacc gacttcgaga agctggagga gtacatcatc 1320
 gacaaggagg acatcgagct gccgtccggc aagcaggagt acctggagtc cctcctcaac 1380
 tcctacatcg tgaagaccat cgccgagctg cgctccgaga aggacgagct gtga 1434

<210> 38

<211> 477

<212> PRT

<213> Thermotoga maritima

<400> 38

Met	Lys	Glu	Thr	Ala	Ala	Ala	Lys	Phe	Glu	Arg	Gln	His	Met	Asp	Ser
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Pro	Asp	Leu	Gly	Thr	Leu	Val	Pro	Arg	Gly	Ser	Met	Ala	Glu	Phe	Phe
					20			25			30				
Pro	Glu	Ile	Pro	Lys	Ile	Gln	Phe	Glu	Gly	Lys	Glu	Ser	Thr	Asn	Pro
					35		40			45					
Leu	Ala	Phe	Arg	Phe	Tyr	Asp	Pro	Asn	Glu	Val	Ile	Asp	Gly	Lys	Pro
					50		55			60					
Leu	Lys	Asp	His	Leu	Lys	Phe	Ser	Val	Ala	Phe	Trp	His	Thr	Phe	Val
					65		70			75			80		
Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly	Asp	Pro	Thr	Ala	Glu	Arg	Pro	Trp
					85		90			95					
Asn	Arg	Phe	Ser	Asp	Pro	Met	Asp	Lys	Ala	Phe	Ala	Arg	Val	Asp	Ala
					100		105			110					
Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu	Asn	Ile	Glu	Tyr	Phe	Cys	Phe	His
					115		120			125					
Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly	Lys	Thr	Leu	Arg	Glu	Thr	Asn	Lys
					130		135			140					
Ile	Leu	Asp	Lys	Val	Val	Glu	Arg	Ile	Lys	Glu	Arg	Met	Lys	Asp	Ser
					145		150			155			160		
Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr	Ala	Asn	Leu	Phe	Ser	His	Pro	Arg
					165		170			175					
Tyr	Met	His	Gly	Ala	Ala	Thr	Thr	Cys	Ser	Ala	Asp	Val	Phe	Ala	Tyr
					180		185			190					
Ala	Ala	Ala	Gln	val	Lys	Lys	Ala	Leu	Glu	Ile	Thr	Lys	Glu	Leu	Gly
					195		200			205					
Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly	Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu
					210		215			220					

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Leu	Asn	Thr	Asp	Leu	Gly	Leu	Glu	Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu
225				230			235								240
Arg	Met	Ala	Val	Glu	Tyr	Ala	Lys	Lys	Ile	Gly	Phe	Thr	Gly	Gln	Phe
				245			250								255
Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu	Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe
				260			265								270
Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe	Leu	Lys	Asn	His	Gly	Leu	Asp	Glu
				275			280								285
Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala	Asn	His	Ala	Thr	Leu	Ala	Gly	His
				290			295								300
Thr	Phe	Gln	His	Glu	Leu	Arg	Met	Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly
				305			310								320
Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp
				325			330								335
Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp	Thr	Thr	Leu	Ala	Met	Tyr	Glu	Val
				340			345								350
Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys	Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys
				355			360								365
val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	Glu	Asp	Leu	Phe	Ile	Gly	His	Ile
				370			375								380
Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu	Gly	Phe	Lys	Ile	Ala	Tyr	Lys	Leu
				385			390								400
Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys	Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser
				405			410								415
Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu	Ile	Val	Glu	Gly	Lys	Thr	Asp	Phe
				420			425								430
Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp	Lys	Glu	Asp	Ile	Glu	Leu	Pro
				435			440								445
Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	Ser	Leu	Leu	Asn	Ser	Tyr	Ile	Val
				450			455								460
Lys	Thr	Ile	Ala	Glu	Leu	Arg	Ser	Glu	Lys	Asp	Glu	Leu			
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<210> 39
<211> 1434
<212> DNA
<213> Thermotoga neapolitana

<400> 39

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gaggcaagg	agtccaccaa	cccgctcgcc	ttcaagttct	acgaccggaa	ggagatcatc	180
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aacgagggcc	gcgacccgtt	cggcgacccg	accgcccggacc	gcccgtggaa	ccgctacacc	300
gaccgatgg	acaaggcctt	cggccgcgtg	gacgcccctt	tcgagttctg	cgagaagctc	360
aacatcgagt	acttctgctt	ccacgaccgc	gacatcgccc	cggaggggcaa	gaccctccgc	420
gagaccaaca	agatcctcga	caaggtggtg	gagcgcata	aggagcgcata	gaaggactcc	480
aacgtgaagc	tcctctgggg	caccgccaac	ctcttctccc	acccgcgcata	catgcacggc	540
gccgccacca	cctgctccgc	cgacgtgttc	gcctacgccc	ccgcccagggt	gaagaaggcc	600
ctggagatca	ccaaggagct	gggcggcgag	ggctacgtgt	tctggggcgg	ccgcgagggc	660
tacgagaccc	tcctcaacac	cgacctcgcc	ttcgagctgg	agaacctcgc	ccgcttcctc	720
cgcatggccg	tggactacgc	caagcgcata	ggcttcacccg	gccagttcct	catcgagccg	780
aagccgaagg	agccgaccaa	gcaccagttac	gacttcgacg	tggccaccgc	ctacgccttc	840
ctcaagtccc	acggcctcga	cgagtacttc	aagttcaaca	tcgaggccaa	ccacgcccacc	900
ctcgccggcc	acaccttcca	gcacgagctg	cgcatggccc	gcatcctcgg	caagctcggc	960
tccatcgacg	ccaaccagggg	cgacctcctc	ctcggctggg	acaccgacca	gttcccgacc	1020
aacgtgtacg	acaccaccc	cgccatgtac	gaggtgatca	aggccggcgg	ttcaccaag	1080
ggccgcctca	acttcgacgc	caaggtgcgc	cgccgcctcct	acaagggtgga	ggaccttttc	1140
atcggccaca	tcgccccat	ggacaccctt	gccctcggt	tcaagggtggc	ctacaagctc	1200
gtgaaggacg	gcgtgctcga	caagttcatc	gaggagaagt	accgctcctt	ccgcgagggc	1260
atcggccgcg	acatcgtgga	gggcaaggtg	gacttcgaga	agctggagga	gtacatcatc	1320
gacaaggaga	ccatcgagct	gccgtccggc	aaggaggat	acctggagtc	cctcatcaac	1380

60110USPCT1 Corrected SEQ LIST 2-2007.txt
tcctacatcg tgaagaccat cctggagctg cgctccgaga aggacgagct gtga 1434

<210> 40
<211> 477
<212> PRT
<213> Thermotoga neapolitana

<400> 40
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20 25 30
Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
35 40 45
Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile Ile Asp Gly Lys Pro
50 55 60
Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
65 70 75 80
Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Asp Arg Pro Trp
85 90 95
Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
100 105 110
Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
115 120 125
Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
130 135 140
Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
145 150 155 160
Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
165 170 175
Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
180 185 190
Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
195 200 205
Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
210 215 220
Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn Leu Ala Arg Phe Leu
225 230 235 240
Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly Phe Thr Gly Gln Phe
245 250 255
Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe
260 265 270
Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser His Gly Leu Asp Glu
275 280 285
Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
290 295 300
Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
305 310 315 320
Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu Gly Trp Asp Thr Asp
325 330 335
Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
340 345 350
Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
355 360 365
Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
370 375 380
Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Val Ala Tyr Lys Leu
385 390 395 400
Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
405 410 415
Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu Gly Lys Val Asp Phe
420 425 430
Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Thr Ile Glu Leu Pro

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435	440	445													
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<211> 1435

<212> DNA

<213> Thermotoga maritima

<400> 41

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 tacgaccgcgaa acgagggtgat cgacggcaag ccgctcaagg accacctaag gttctccgtg 240
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 cgcggcgatc accgcttctc cgacccgatg gacaaggcct tcgccccgt ggacgcccctc 360
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 gctggaggag tacatcatcg acaaggagga catcgagctg ccgtccggca agcaggagta 1380
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<210> 42

<211> 478

<212> PRT

<213> Thermotoga maritima

<400> 42

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				20			25				30				
Ile	Pro	Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Ile	Gln	Phe	Glu
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				65			70				75			80	
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				85			90				95				
Pro	Thr	Ala	Glu	Arg	Pro	Trp	Asn	Arg	Phe	Ser	Asp	Pro	Met	Asp	Lys
				100			105				110				
Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu	Asn
				115			120				125				
Ile	Glu	Tyr	Phe	Cys	Phe	His	Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly	Lys
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Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe	Leu
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Lys	Asn	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala	Asn
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His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met	Ala
				305					310				315		320
Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu
				325					330				335		
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				385					390				395		400
Phe	Lys	Ile	Ala	Tyr	Lys	Leu	Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys	Phe
				405					410				415		
Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu	Ile
				420					425				430		
Val	Glu	Gly	Lys	Thr	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp
				435					440				445		
Lys	Glu	Asp	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	Ser
				450					455				460		
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<210> 43

<211> 1436

<212> DNA

<213> Thermotoga neapolitana

<400> 43

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<211> 478

<212> PRT

<213> Thermotoga neapolitana

<400> 44

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Ile	Pro	Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Val	Gln	Phe	Glu
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				50				55				60			
Glu	Ile	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser	Val
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Ala	Phe	Trp	His	Thr	Phe	Val	Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly	Asp
				85				90				95			
Pro	Thr	Ala	Asp	Arg	Pro	Trp	Asn	Arg	Tyr	Thr	Asp	Pro	Met	Asp	Lys
				100				105				110			
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				115				120				125			
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				130				135				140			
Thr	Leu	Arg	Glu	Thr	Asn	Lys	Ile	Leu	Asp	Lys	Val	Val	Glu	Arg	Ile
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Lys	Glu	Arg	Met	Lys	Asp	Ser	Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr	Ala
				165				170				175			
Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr	Cys
				180				185				190			
Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala	Leu
				195				200				205			
Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly	Gly
				210				215				220			
Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Phe	Glu	Leu
				225				230				235			240
Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Asp	Tyr	Ala	Lys	Arg
				245				250				255			
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				260				265				270			
Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe	Leu
				275				280				285			
Lys	Ser	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala	Asn
				290				295				300			
His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met	Ala
				305				310				315			320
Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu
				325				330				335			
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				340				345				350			
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				355				360				365			

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Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	Glu
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385					390				395					400	
Phe	Lys	Val	Ala	Tyr	Lys	Leu	Val	Lys	Asp	Gly	Val	Leu	Asp	Lys	Phe
					405				410				415		
Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Arg	Glu	Gly	Ile	Gly	Arg	Asp	Ile
					420			425				430			
val	Glu	Gly	Lys	Val	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp
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Lys	Glu	Thr	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	Ser
					450			455				460			
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<210> 45

<211> 1095

<212> PRT

<213> Aspergillus shirousami

<400> 45

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					20			25					30		
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Leu	Asp	Tyr	Ile	Gln	Gly	Met	Gly	Phe	Thr	Ala	Ile	Trp	Ile	Thr	Pro
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Gly	Tyr	Trp	Gln	Gln	Asp	Ile	Tyr	Ser	Leu	Asn	Glu	Asn	Tyr	Gly	Thr
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Gly	Ser	Ser	Val	Asp	Tyr	Ser	Val	Phe	Lys	Pro	Phe	Ser	Ser	Gln	Asp
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Tyr	Phe	His	Pro	Phe	Cys	Phe	Ile	Gln	Asn	Tyr	Glu	Asp	Gln	Thr	Gln
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Val	Glu	Asp	Cys	Trp	Leu	Gly	Asp	Asn	Thr	val	Ser	Leu	Pro	Asp	Leu
					165			170				175			
Asp	Thr	Thr	Lys	Asp	val	val	Lys	Asn	Glu	Trp	Tyr	Asp	Trp	Val	Gly
					180			185				190			
Ser	Leu	val	Ser	Asn	Tyr	Ser	Ile	Asp	Gly	Leu	Arg	Ile	Asp	Thr	val
					195			200				205			
Lys	His	Val	Gln	Lys	Asp	Phe	Trp	Pro	Gly	Tyr	Asn	Lys	Ala	Ala	Gly
					210			215				220			
val	Tyr	Cys	Ile	Gly	Glu	Val	Leu	Asp	Val	Asp	Pro	Ala	Tyr	Thr	Cys
					225			230				235			240
Pro	Tyr	Gln	Asn	val	Met	Asp	Gly	val	Leu	Asn	Tyr	Pro	Ile	Tyr	Tyr
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Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser	Gly	Ser	Met	Asp	Asp	Leu
					260			265				270			
Tyr	Asn	Met	Ile	Asn	Thr	val	Lys	Ser	Asp	Cys	Pro	Asp	Ser	Thr	Leu
					275			280				285			
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					290			295				300			
Thr	Asn	Asp	Ile	Ala	Leu	Ala	Lys	Asn	Val	Ala	Ala	Phe	Ile	Ile	Leu
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Asn	Asp	Gly	Ile	Pro	Ile	Ile	Tyr	Ala	Gly	Gln	Glu	Gln	His	Tyr	Ala

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Gly	Gly	Asn	Asp	Pro	Ala	Asn	Arg	Glu	Ala	Thr	Trp	Leu	Ser	Gly	Tyr
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Pro	Thr	Asp	Ser	Glu	Leu	Tyr	Lys	Leu	Ile	Ala	Ser	Ala	Asn	Ala	Ile
340					355			360					365		
Arg	Asn	Tyr	Ala	Ile	Ser	Lys	Asp	Thr	Gly	Phe	Val	Thr	Tyr	Lys	Asn
355						370		375				380			
Trp	Pro	Ile	Tyr	Lys	Asp	Asp	Thr	Thr	Ile	Ala	Met	Arg	Lys	Gly	Thr
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Asp	Gly	Ser	Gln	Ile	Val	Thr	Ile	Leu	Ser	Asn	Lys	Gly	Ala	Ser	Gly
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Asp	Ser	Tyr	Thr	Leu	Ser	Leu	Ser	Gly	Ala	Gly	Tyr	Thr	Ala	Gly	Gln
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														425	
Gln	Leu	Thr	Glu	Val	Ile	Gly	Cys	Thr	Thr	Val	Thr	Val	Gly	Ser	Asp
415					420			425			430			435	
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Gly	Asn	Val	Pro	Val	Pro	Met	Ala	Gly	Gly	Leu	Pro	Arg	Val	Leu	Tyr
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														445	
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445					450			455			460			465	
														470	
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465					470			475			480			485	
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Asp	Ser	Gly	Ile	Val	Val	Ala	Ser	Pro	Ser	Thr	Asp	Asn	Pro	Asp	Tyr
485					490			495			500			505	
														510	
Phe	Tyr	Thr	Trp	Thr	Arg	Asp	Ser	Gly	Ile	Val	Leu	Lys	Thr	Leu	Val
495					500			505			510			515	
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Gly	Tyr	Thr	Ser	Ala	Ala	Thr	Glu	Ile	Val	Trp	Pro	Leu	Val	Arg	Asn
595					600			605			610			615	
														620	
Asp	Leu	Ser	Tyr	Val	Ala	Gln	Tyr	Trp	Asn	Gln	Thr	Gly	Tyr	Asp	Leu
610					615			620			625			630	
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Trp	Glu	Glu	Val	Asn	Gly	Ser	Ser	Phe	Phe	Thr	Ile	Ala	Val	Gln	His
605					610			615			620			625	
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Arg	Ala	Leu	Val	Glu	Gly	Ser	Ala	Phe	Ala	Thr	Ala	Val	Gly	Ser	Ser
625					630			635			640			645	
														650	
Cys	Ser	Trp	Cys	Asp	Ser	Gln	Ala	Pro	Gln	Ile	Leu	Cys	Tyr	Leu	Gln
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615					620			625			630			635	
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610					615			620			625			630	
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585					590			595			600			605	
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865			870					875				880			
Phe	Asp	Lys	Ser	Asp	Gly	Asp	Glu	Leu	Ser	Ala	Arg	Asp	Leu	Thr	Trp
	885				890				895						
Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Ala	Asn	Asn	Arg	Arg	Asn	Ser	Val	Val
				900				905				910			
Pro	Pro	Ser	Trp	Gly	Glu	Thr	Ser	Ala	Ser	Ser	Val	Pro	Gly	Thr	Cys
	915			920				925							
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Thr	Gly	Ser	Gly	Gly	Val	Thr	Ser	Thr	Ser	Lys	Thr	Thr	Thr	Thr	Ala
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Ser	Lys	Thr	Ser	Thr	Thr	Ser	Ser	Thr	Ser	Cys	Thr	Thr	Pro	Thr	
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Ser	Asp	Gly	Ile	Ala	Leu	Ser	Ala	Asp	Lys	Tyr	Thr	Ser	Ser	Asn	Pro
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<213> Aspergillus shirousami

<400> 46

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<211> 679

<212> PRT

<213> Thermoanaerobacterium thermosaccharolyticum

<400> 47

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Ser	Ala	Arg	Gly	Asn	Ile	Ile	Glu	Gly	Ala	Glu	Ile	Asp	Leu	Thr	Lys
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Asn	Phe	Asn	Gly	Lys	Ala	Asn	Ser	Leu	Tyr	Tyr	Asn	Ser	Met	Met	Ile
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Tyr	His	Leu	Val	Trp	Ser	Arg	Asp	Leu	Tyr	His	Val	Ala	Asn	Ala	Phe
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355				360						365					
Ala	Lys	Val	Val	Lys	Asp	Asn	Gly	Met	Ile	Pro	Gln	Asn	Thr	Trp	Ile
370				375						380					
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Ala	Glu	Tyr	Val	Ile	Leu	Phe	Ala	Ser	Asn	Ile	Glu	His	Lys	Val	Leu
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675

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 Ser Asn Tyr Glu Tyr Trp Thr Phe Ser Ala Ser Ile Asn Gly Ile Lys
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tccctcgccg aggagttcga ccgcaccacc ggcctctcca ccggcgcccc cgacctcacc 1680
tggtcccacg cctccctcat caccgcctcc tacgccaagg ccggcgcccc ggccgccc 1737

<210> 51
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 51
Met Ala Lys His Leu Ala Ala Met Cys Trp Cys Ser Leu Leu Val Leu
1 5 10 15
Val Leu Leu Cys Leu Gly Ser Gln Leu Ala Gln Ser Gln Val Leu Phe
20 25 30
Gln Gly Phe Asn Trp Glu Ser Trp Lys Lys Gln Gly Gly Trp Tyr Asn
35 40 45
Tyr Leu Leu Gly Arg Val Asp Asp Ile Ala Ala Thr Gly Ala Thr His
50 55 60
Val Trp Leu Pro Gln Pro Ser His Ser Val Ala Pro Gln Gly Tyr Met
65 70 75 80
Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser Lys Tyr Gly Thr His Ala
85 90 95
Glu Leu Lys Ser Leu Thr Ala Ala Phe His Ala Lys Gly Val Gln Cys
100 105 110
Val Ala Asp Val Val Ile Asn His Arg Cys Ala Asp Tyr Lys Asp Gly
115 120 125

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Arg	Gly	Ile	Tyr	Cys	Val	Phe	Glu	Gly	Gly	Thr	Pro	Asp	Ser	Arg	Leu
130					135					140					
Asp	Trp	Gly	Pro	Asp	Met	Ile	Cys	Ser	Asp	Asp	Thr	Gln	Tyr	Ser	Asn
145					150				155						160
Gly	Arg	Gly	His	Arg	Asp	Thr	Gly	Ala	Asp	Phe	Ala	Ala	Ala	Pro	Asp
					165			170						175	
Ile	Asp	His	Leu	Asn	Pro	Arg	Val	Gln	Gln	Glu	Leu	Ser	Asp	Trp	Leu
					180			185						190	
Asn	Trp	Leu	Lys	Ser	Asp	Leu	Gly	Phe	Asp	Gly	Trp	Arg	Leu	Asp	Phe
					195			200				205			
Ala	Lys	Gly	Tyr	Ser	Ala	Ala	val	Ala	Lys	val	Tyr	Val	Asp	Ser	Thr
					210			215				220			
Ala	Pro	Thr	Phe	Val	Val	Ala	Glu	Ile	Trp	Ser	Ser	Leu	His	Tyr	Asp
					225			230		235				240	
Gly	Asn	Gly	Glu	Pro	Ser	Ser	Asn	Gln	Asp	Ala	Asp	Arg	Gln	Glu	Leu
					245			250				255			
val	Asn	Trp	Ala	Gln	Ala	Val	Gly	Gly	Pro	Ala	Ala	Ala	Phe	Asp	Phe
					260			265				270			
Thr	Thr	Lys	Gly	val	Leu	Gln	Ala	Ala	val	Gln	Gly	Glu	Leu	Trp	Arg
					275			280				285			
Met	Lys	Asp	Gly	Asn	Gly	Lys	Ala	Pro	Gly	Met	Ile	Gly	Trp	Leu	Pro
					290			295				300			
Glu	Lys	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Gly	Ser	Thr	Gln
					305			310			315			320	
Asn	Ser	Trp	Pro	Phe	Pro	Ser	Asp	Lys	Val	Met	Gln	Gly	Tyr	Ala	Tyr
					325			330				335			
Ile	Leu	Thr	His	Pro	Gly	Thr	Pro	Cys	Ile	Phe	Tyr	Asp	His	Val	Phe
					340			345				350			
Asp	Trp	Asn	Leu	Lys	Gln	Glu	Ile	Ser	Ala	Leu	Ser	Ala	val	Arg	Ser
					355			360				365			
Arg	Asn	Gly	Ile	His	Pro	Gly	Ser	Glu	Leu	Asn	Ile	Leu	Ala	Ala	Asp
					370			375			380				
Gly	Asp	Leu	Tyr	Val	Ala	Lys	Ile	Asp	Asp	Lys	Val	Ile	val	Lys	Ile
					385			390			395			400	
Gly	Ser	Arg	Tyr	Asp	val	Gly	Asn	Leu	Ile	Pro	Ser	Asp	Phe	His	Ala
					405			410				415			
val	Ala	His	Gly	Asn	Asn	Tyr	Cys	Val	Trp	Glu	Lys	His	Gly	Leu	Arg
					420			425				430			
val	Pro	Ala	Gly	Arg	His	His									
					435										

<210> 52
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 52
atggcgaagc acttggctgc catgtgctgg tgcagccccc tagtgcttgt actgctctgc 60
ttgggctccc agctggccca atccccaggc ctcttccagg gttcaactg ggagtctgtgg 120
aagaagcaag gtgggtggta caactaccc tcggggcgcc tggacgacat cgccgcgcacg 180
ggggccacgc acgtctggct cccgcaggcc tcgcactcgg tggcgccgca ggggtacatg 240
cccgcccgcc tctacgacct ggacgcgtcc aagtacggca cccacgcggc gctcaagtgc 300
ctcacccgcgg cgttccacgc caagggcgtc cagtgcgtcg ccgacgtcgt gatcaaccac 360
cgctgcgcgg actacaagga cggccgcggc atctactgcg tcttcgaggc cggcacgc 420
gacagccgcc tcgactgggg ccccgacatg atctgcagcg acgacacgcgt gtactccaac 480
gggcgcgggc accgcgacac gggggccgac ttgcggcccg cggccgcacat cgaccaccc 540
aacccgcgcg tgcaagcagga gctctcgac tggctcaact ggctcaagtc cgacccgtgc 600
ttcgacggct ggcgcctcga cttcgccaag ggctactccg ccggccgtcgc caagggtgtac 660
gtcgacagca ccgcggccac cttcgctcgtc gccgagatat ggagctccct ccactacgc 720

60110USPCT1 Corrected SEQ LIST 2-2007.txt

ggcaacggcg agccgtccag caaccaggac gccgacaggc aggagctggc caactggcg 780
caggcggtgg gcggccccgc cgccgcgttc gacttcacca ccaagggcg tgcaggcg 840
gccgtccagg gcgagctgtg ggcgtcatgaag gacggcaacg gcaaggcgcc cggatgatc 900
ggctggctgc cggagaaggc cgtcacgttc gtcgacaacc acgacaccgg ctccacgcag 960
aactcggtgc cattccccctc cgacaaggc atgcaggcgt acgcctataat cctcacgcac 1020
ccaggaactc catgcacatctt ctacgaccac gtttcgact ggaacctgaa gcaggagatc 1080
agcgcgtgt ctgcggtgag gtcaagaaac gggatccacc cggggagcga gctgaacatc 1140
ctcgccgccc acggggatct ctacgtcgcc aagattgacg acaaggcatc cgtgaagatc 1200
gggtcacggc acgacgtcgg gaacctgatc ccctcagact tccacgcccgt tgcccctggc 1260
aacaactact gcgtttggga gaagcacggc ctgagagttc cagcggcg gcaccactag 1320

<210> 53

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 53

Ala Thr Gly Gly Thr Thr Ala Thr Thr Gly Ser Gly Gly
1 5 10 15
Val Thr Ser Thr Ser Lys Thr Thr Ala Ser Lys Thr Ser Thr
20 25 30
Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val
35 40 45

<210> 54

<211> 137

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 54

gccaccggcg gcaccaccac caccgcacc accaccggct ccggcggcg tgcacc 60
tccaagacca ccaccaccgc ctccaagacc tccaccacca ctcctccac ctcctgcacc 120
accccgaccg ccgtgtc 137

<210> 55

<211> 300

<212> PRT

<213> Pyrococcus furiosus

<400> 55

Ile Tyr Phe Val Glu Lys Tyr His Thr Ser Glu Asp Lys Ser Thr Ser
1 5 10 15
Asn Thr Ser Ser Thr Pro Pro Gln Thr Thr Leu Ser Thr Thr Lys Val
20 25 30
Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly Ala Pro Ile
35 40 45
Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu Ile Asn Leu
50 55 60
Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr Tyr Asn Leu
65 70 75 80
Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn Ile Val Leu
85 90 95
Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile Phe Tyr Gly
100 105 110
Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro Ile Pro Leu
115 120 125

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Pro	Ser	Lys	Val	Ser	Asn	Leu	Thr	Asp	Phe	Tyr	Leu	Thr	Ile	Ser	Tyr
130						135					140				
Lys	Leu	Glu	Pro	Lys	Asn	Gly	Leu	Pro	Ile	Asn	Phe	Ala	Ile	Glu	Ser
145						150				155					160
Trp	Leu	Thr	Arg	Glu	Ala	Trp	Arg	Thr	Thr	Gly	Ile	Asn	Ser	Asp	Glu
						165			170					175	
Gln	Glu	Val	Met	Ile	Trp	Ile	Tyr	Tyr	Asp	Gly	Leu	Gln	Pro	Ala	Gly
			180				185					190			
Ser	Lys	Val	Lys	Glu	Ile	Val	Val	Pro	Ile	Ile	Val	Asn	Gly	Thr	Pro
			195			200					205				
Val	Asn	Ala	Thr	Phe	Glu	Val	Trp	Lys	Ala	Asn	Ile	Gly	Trp	Glu	Tyr
			210			215					220				
Val	Ala	Phe	Arg	Ile	Lys	Thr	Pro	Ile	Lys	Glu	Gly	Thr	Val	Thr	Ile
			225		230				235				240		
Pro	Tyr	Gly	Ala	Phe	Ile	Ser	Val	Ala	Ala	Asn	Ile	Ser	Ser	Leu	Pro
						245			250				255		
Asn	Tyr	Thr	Glu	Leu	Tyr	Leu	Glu	Asp	Val	Glu	Ile	Gly	Thr	Glu	Phe
					260			265			270				
Gly	Thr	Pro	Ser	Thr	Thr	Ser	Ala	His	Leu	Glu	Trp	Trp	Ile	Thr	Asn
					275			280			285				
Ile	Thr	Leu	Thr	Pro	Leu	Asp	Arg	Pro	Leu	Ile	Ser				
					290			295			300				

<210> 56

<211> 903

<212> DNA

<213> Pyrococcus furiosus

<400> 56

atctacttcg	tggagaagta	ccacaccc	gaggacaagt	ccac	cacc	cctccaa	cac	cctcc	60
acc	cccgcgc	agaccacc	ctcc	aagg	tgctca	agat	ccgc	gttctacatc	120
ggc	gagtggc	ccggcgcccc	gatcgaca	gacggcgac	gcaacc	cgga	gttctacatc	180	
gag	atcaacc	tctggAACAT	cctcaacg	accggcttc	ccgagatgac	ctacaac	c	240	
act	atggcg	tgctccacta	cgtc	cagcag	ctcgaca	tcgt	gtcc	cgaccgctcc	300
aact	gggtgc	acggctaccc	gaaat	ttc	tacggca	agcc	gtggaa	cgccaactac	360
gcc	accgcac	gccc	gatccc	gctccgtcc	aagg	gttcca	ac	tttctac	420
acc	atctc	acta	gctc	gatccc	gttctcc	tc	acttc	tc	480
at	ctggat	acta	cgac	cc	gcccgttcca	agg	gttga	gatcg	540
ccg	atcatcg	tga	acggc	cc	ggcttcca	agg	gttggaa	ggcca	600
gg	cttggagt	acgtggc	cc	catca	ccccc	agg	ggggcac	cgtgaccatc	660
ccg	tacggcg	cc	catca	cc	gttcca	agg	ggggcac	720	780
aag	tac	aggacgtg	gg	gatcg	cc	gttcca	cc	ctacacc	840
cac	tcg	aggacgtg	g	gatcg	cc	gttcca	cc	tcacacc	900
tt	ggat	ggat	cac	atc	cc	gttcca	cc	tcacacc	903

<210> 57

<211> 387

<212> PRT

<213> Thermus flavus

<400> 57

Met	Tyr	Glu	Pro	Lys	Pro	Glu	His	Arg	Phe	Thr	Phe	Gly	Leu	Trp	Thr
1							10					15			
Val	Asp	Asn	Val	Asp	Arg	Asp	Pro	Phe	Gly	Asp	Thr	Val	Arg	Glu	Arg
							20			25			30		
Leu	Asp	Pro	Val	Tyr	val	val	His	Lys	Leu	Ala	Glu	Leu	Gly	Ala	Tyr
							35			40			45		
Gly	Val	Asn	Leu	His	Asp	Glu	Asp	Leu	Ile	Pro	Arg	Gly	Thr	Pro	Pro
							50			55			60		
Gln	Glu	Arg	Asp	Gln	Ile	Val	Arg	Arg	Phe	Lys	Lys	Ala	Leu	Asp	Glu
							65			70			75		80

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Thr Val Leu Lys Val Pro Met Val Thr Ala Asn Leu Phe Ser Glu Pro
 85 90 95
 Ala Phe Arg Asp Gly Ala Ser Thr Thr Arg Asp Pro Trp Val Trp Ala
 100 105 110
 Tyr Ala Leu Arg Lys Ser Leu Glu Thr Met Asp Leu Gly Ala Glu Leu
 115 120 125
 Gly Ala Glu Ile Tyr Met Phe Trp Met Val Arg Glu Arg Ser Glu Val
 130 135 140
 Glu Ser Thr Asp Lys Thr Arg Lys Val Trp Asp Trp Val Arg Glu Thr
 145 150 155 160
 Leu Asn Phe Met Thr Ala Tyr Thr Glu Asp Gln Gly Tyr Gly Tyr Arg
 165 170 175
 Phe Ser Val Glu Pro Lys Pro Asn Glu Pro Arg Gly Asp Ile Tyr Phe
 180 185 190
 Thr Thr Val Gly Ser Met Leu Ala Leu Ile His Thr Leu Asp Arg Pro
 195 200 205
 Glu Arg Phe Gly Leu Asn Pro Glu Phe Ala His Glu Thr Met Ala Gly
 210 215 220
 Leu Asn Phe Asp His Ala Val Ala Gln Ala Val Asp Ala Gly Lys Leu
 225 230 235 240
 Phe His Ile Asp Leu Asn Asp Gln Arg Met Ser Arg Phe Asp Gln Asp
 245 250 255
 Leu Arg Phe Gly Ser Glu Asn Leu Lys Ala Gly Phe Phe Leu Val Asp
 260 265 270
 Leu Leu Glu Ser Ser Gly Tyr Gln Gly Pro Arg His Phe Glu Ala His
 275 280 285
 Ala Leu Arg Thr Glu Asp Glu Glu Gly Val Trp Thr Phe Val Arg Val
 290 295 300
 Cys Met Arg Thr Tyr Leu Ile Ile Lys Val Arg Ala Glu Thr Phe Arg
 305 310 315 320
 Glu Asp Pro Glu Val Lys Glu Leu Leu Ala Ala Tyr Tyr Gln Glu Asp
 325 330 335
 Pro Ala Thr Leu Ala Leu Leu Asp Pro Tyr Ser Arg Glu Lys Ala Glu
 340 345 350
 Ala Leu Lys Arg Ala Glu Leu Pro Leu Glu Thr Lys Arg Arg Arg Gly
 355 360 365
 Tyr Ala Leu Glu Arg Leu Asp Gln Leu Ala Val Glu Tyr Leu Leu Gly
 370 375 380
 Val Arg Gly
 385

<210> 58
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 58
 atgggaaaga acggcaacct gtgctgcttc tctctgctgc tgcttcttct cggccgggttg 60
 gcgtccggcc atcaaatcta cttcgtggag aagtaccaca cctccgaggca caagtccacc 120
 tccaaacacct cctccacccc gccgcagacc accctctcca ccaccaaggt gctcaagatc 180
 cgctacccgg acgacggta gttggcccgcc gccccgatcg acaaggacgg cgacggcaac 240
 ccggagttct acatcgagat caacctctgg aacatcctca acgcccacccgg cttcgccgag 300
 atgacctaca acctcactag tggcgtgctc cactacgtgc agcagctcga caacatcgtg 360
 ctccgcgacc gctccaaactg ggtgcacggc taccggaaa ttttctacgg caacaagccg 420
 tggAACGCCA actacgccac cgacggcccg atcccgctcc cgtccaaagggt gtccaaacctc 480
 accgacttct acctcaccat ctcctacaag ctcgagccga agaacggctc cccgatcaac 540
 ttgcgcattcg agtcctggct cacccgcgag gcctggcgca ccaccggcat caactccgac 600
 gagcaggagg tggatgtctg gatctactac gacggcctcc agcccgcggg ctccaagggtg 660
 aaggagatcg tggtgccgat catcgtgaac ggcaccccg gtaacgccac cttcgaggtg 720

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tggaggcca acatcggtcg ggagtacgtg gccttccgca tcaagacccc gatcaaggag 780
ggaccgtga ccatcccgta cgccgccttc atctccgtgg ccgccaacat ctccctccctc 840
ccgaactaca ccgagaagta cctcgaggac gtggagatcg gcaccgagtt cggcacccccg 900
tccaccacct cggcccacct cgagtggtgg atcaccaaca tcaccctcac cccgctcgac 960
cgcccgctca tctccttag 978

<210> 59

<211> 1920

<212> DNA

<213> Aspergillus niger

<400> 59

atgtccttcc gctccctcct cgccctctcc ggcctcggt gcaccggcct cgccaaacgtg 60
atctccaagc gcgccaccct cgactcctgg ctctccaacg aggccaccgt ggcccgccacc 120
gccatcctca acaacatcg cgccgacggc gcctgggtgt ccggcgccga ctccggcattc 180
gtggtggcct ccccgtccac cgacaacccg gactacttct acacctggac ccgcgactcc 240
ggcctcggtgc tcaagaccct cgtggacccct ttccgcaacg ggcacacccctc cttccctctcc 300
accatcgaga actacatctc cgcccagggc atcgtgcagg gcatctccaa cccgtccggc 360
gacctctcct ccggcgccgg cctcggcgag ccgaagttca acgtggacga gaccgcctac 420
accggctcct ggggcccggcc gcagcgcgac ggcccggccc tccgcgcccac cgccatgatc 480
ggcttcggcc agtggctcct cgacaacccg tacacctcca ccgcaccga catcggtgg 540
ccgctcggtgc gcaacgaccc ttcctacgtg gcccagtact ggaaccagac cggctacgac 600
ctctggagg aggtgaacgg ctcctccctc ttaccatcg ccgtgcagca cccgcgcctc 660
gtggagggct ccgccttcgc caccggcgtg ggctccctt gctcctggc cgactcccg 720
gccccggaga tcctctgcta cctccagttcc ttctggaccg gctccttcat cctcgccaaac 780
ttcgactcct cccgctccgg caaggacgcc aacaccctcc tcggctccat ccacacccctc 840
gaccggagg ccgcctgcga cgactccacc ttccagccgt gctcccccgc cgccctcgcc 900
aaccacaagg aggtggtgaa ctccttccgc tccatctaca ccctcaacga cggcctctcc 960
gactccgagg ccgtggccgt gggccgctac ccggaggaca cctactacaa cggcaacccg 1020
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aagcagggt ccctcgaggt gaccgacgtg tccctcgact tcttcaaggc cctctactcc 1140
gacgcccaca ccggcaccta ctccctccctc tcctccaccc actcctccat cgtggacgcc 1200
gtgaagaccc tcgcccacgg cttcggttcc atcgtggaga cccacccgc ctccaaacggc 1260
tccatgtccg agcagtacga caagtccgac ggcgagcagc tctccggcccg cgacccatcacc 1320
tggtcctacg ccgcctcctt caccggccaa aaccggccgc actccgttgt gccggctcc 1380
tggggcgaga cctccgcctc ctccgtggcg ggcacccgc ccgcacccctc cgccatcgcc 1440
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accaccgcca ccccgaccgg ctccggctcc gtgacccctca cctccaagac caccggccacc 1560
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gtgacccctcg acctcaccgc caccaccacc tacggcgaga acatctaccc cgtggctcc 1680
atctcccaac tcggcgactg ggagacccctc gacggcatcg ccctctccgc cgacaaagtac 1740
acctccctcg acccgctctg gtacgtgacc gtgacccctcc cggccggcga gtccttcgag 1800
tacaagttca tccgcacatcg gtccgacgac tccgtggagt gggagttccga cccgaaccgc 1860
gagtacaccg tgccgcaggc ctgcggcacc tccaccgcca ccgtgaccga caccctggcgc 1920

<210> 60

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 60

Ser Glu Lys Asp Glu Leu

1

5

<210> 61

<211> 561

<212> DNA

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<213> Artificial Sequence

<220>

<223> Xylanase BD7436

<220>

<221> CDS

<222> (1)..(561)

<400> 61

atg gct agc acc ttc tac tgg cat ttg tgg acc gac ggc atc ggc acc	48
Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr	
1 5 10 15	

gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc	96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser	
20 25 30	

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct	144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala	
35 40 45	

acc agg gtg atc aac tac aac gct cat gct ttc agc gtg gtg ggc aac	192
Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn	
50 55 60	

gct tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac	240
Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr	
65 70 75 80	

tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag	288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys	
85 90 95	

ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc	336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr	
100 105 110	

agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa	384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln	
115 120 125	

ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc	432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr	
130 135 140	

atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac	480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn	
145 150 155 160	

ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa	528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln	
165 170 175	

agc agc ggc tac agc aac gtg acc gtg tgg tag	561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp	
180 185	

<210> 62

<211> 186

<212> PRT

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 62

Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
50 55 60

Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 63

<211> 561

<212> DNA

<213> Artificial Sequence

<220>

<223> xylanase BD6002A

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>
<221> CDS
<222> (1)..(561)

<400> 63

atg gct agc acc gac tac tgg caa aac tgg acc gac ggc ggc ggc acc	48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr	
1 5 10 15	
gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc	96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser	
20 25 30	
aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct	144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala	
35 40 45	
acc agg gtg atc aac tac aac gct ggc gct ttc agc cca agc ggc aac	192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn	
50 55 60	
ggc tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac	240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr	
65 70 75 80	
tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag	288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys	
85 90 95	
ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc	336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr	
100 105 110	
agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa	384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln	
115 120 125	
ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc	432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr	
130 135 140	
atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac	480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn	
145 150 155 160	
ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa	528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln	
165 170 175	
agc agc ggc tac agc aac gtg acc gtg tgg tag	561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp	
180 185	

<210> 64
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 64

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 65

<211> 561

<212> DNA

<213> Artificial sequence

<220>

<223> xylanase BD6002B

<220>

<221> CDS

<222> (1)..(561)

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 65		
atg gcc tcc acc gac tac tgg cag aac tgg acc gac ggc ggc ggc acc		48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr		
1 5 10 15		
gtg aac gcc acc aac ggc tcc gac ggc aac tac tcc gtg tcc tgg tcc		96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser		
20 25 30		
aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc tcc gcc		144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala		
35 40 45		
acc cgc gtg atc aac tac aac gcc ggc gcc ttc tcc ccg tcc ggc aac		192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn		
50 55 60		
ggc tac ctc gcc ctc tac ggc tgg acc cgc aac tcc ctc atc gag tac		240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr		
65 70 75 80		
tac gtg gtg gac tcc tgg ggc acc tac cgc ccg acc ggc acc tac aag		288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys		
85 90 95		
ggc acc gtg acc tcc gac ggc ggc acc tac gac atc tac acc acc acc		336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr		
100 105 110		
cgc acc aac gcc ccg tcc atc gac ggc aac aac acc acc ttc acc cag		384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln		
115 120 125		
ttc tgg tcc gtg cgc cag tcc aag cgc ccg atc ggc acc aac aac acc		432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr		
130 135 140		
atc acc ttc tcc aac cac gtg aac gcc tgg aag tcc aag ggc atg aac		480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn		
145 150 155 160		
ctc ggc tcc tcc tgg tcc tac cag gtg ctc gcc acc gag ggc tac cag		528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln		
165 170 175		
tcc tcc ggc tac tcc aac gtg acc gtg tgg tga		561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp		
180 185		

<210> 66
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 66

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr

1 5 10 15

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 67
<211> 2071
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(2071)
<223> Promoter

<400> 67
tccatgctgt cctactactt gcttcatccc cttctacatt ttgttctggc ttttggcctg 60
catttcgat catgatgtat gtgatttcca atctgctgca atatgaatgg agactctgtg 120
ctaaccatca acaacatgaa atgcttatga ggccttgct gagcagccaa tcttgccgt 180

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gttatgtct tcacaggccg aattcctctg tttgtttt caccctcaat atttggaaac	240
atttatctag gttgttgta tccaggccta taaatcatac atgatgtgt cgtattggat	300
gtaatgtgg tggcggttc agtgccttgg atttgagttt gatgagagtt gcttctgggt	360
caccactcac cattatcgat gctcctcttc agcataaggt aaaagtcttc cctgtttacg	420
ttatTTacc cactatggtt gcttgggttg gtttttcct gattgcttat gccatggaaa	480
gtcattttagt atgttgaact tgaattaact gtagaattgt atacatgttc catttgtt	540
gtacttcctt ctttctatt agtagcctca gatgagtgtg aaaaaaacag attatataac	600
ttgccctata aatcatttga aaaaaatatt gtacagttag aaattgatat atagtgaatt	660
tttaagagca tgTTTccta aagaagtata tattttctat gtacaaaggc cattgaagta	720
attgttagata caggataatg tagactttt ggacttacac tgctaccctt aagtaacaat	780
catgagcaat agtgttgcaa tgatatttag gctgcattcg tttactctct tgatttccat	840
gagcacgctt cccaaactgt taaactctgt gtttttgcc aaaaaaaaaat gcataggaaa	900
gttgctttta aaaaatcata tcaatccatt tttaagttt tagctaatac ttaattaatc	960
atgcgctaatt aagtcaactt gttttcgta ctagagagat tgTTTgaac cagcactcaa	1020
gaacacagcc ttaacccagc caaataatgc tacaacctac cagtccacac ctcttgtaaa	1080
gcatttggc catggaaaag ctaagatgac agcaacctgt tcaggaaaac aactgacaag	1140
gtcatagggc gagggagctt ttggaaaggt gccgtgcagt tcaaacaatt agttagcagt	1200
agggtgttgg ttttgctca cagcaataag aagttaatca tggtaggc aacccaaata	1260
aaacacccaa atatgcacaa ggcagttgt tgtattctgt agtacagaca aaactaaaag	1320
taatgaaaga agatgtggc tttagaaaagg aaacaatatac atgagtaatg tgtggcatt	1380
atgggaccac gaaataaaaaa gaacattttg atgagtcgtg tatttcgtat gagcctcaaa	1440
agttctctca ccccgataa gaaaccctta agcaatgtgc aaagttgca ttctccactg	1500
acataatgca aaataagata tcatcgatga catagcaact catgcacat atcatgcctc	1560
tctcaaccta ttcattccta ctcatctaca taagtatctt cagctaaatg tttagaacata	1620
aacccataag tcacgttgc tgagtattag gcgtgacaca tgacaaatca cagactcaag	1680
caagataaaatgatg tgtacataaa actccagagc tatatgtcat attgcaaaaa	1740
gaggagagct tataagacaa ggcacgtactc aaaaaattc atttgcctt cgtgtcaaaa	1800
agaggagggc ttacattat ccatgtcata ttgaaaaaaga aagagagaaa gaacaacaca	1860
atgctgcgtc aattatacat atctgtatgt ccatcattat tcatccaccc ttcgtgtacc	1920
acacttcata tatcatgagt cacttcgtt ctggacatta acaaactcta tcttaacatt	1980
tagatgcaag agcctttatc tcactataaa tgcacgtga tttctcattt tttctcacaa	2040
aaagcattca gttcattttt cctacaacaa c	2071

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<210> 68
<211> 79
<212> PRT
<213> zea mays

<220>
<221> SIGNAL
<222> (1)..(79)
<223> Maize waxy signal sequence.

<400> 68

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1 5 10 15

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20 25 30

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35 40 45

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50 55 60

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala
65 70 75

<210> 69
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic Bromelain sequence

<220>
<221> CDS
<222> (1)..(1005)
<223> Synthetic Bromelain

<400> 69
atg gcc tgg aag gtg cag gtg gtg ttc ctc ttc ctc ttc ctc tgc gtg 48
Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1 5 10 15

atg tgg gcc tcc ccg tcc gcc tcc gcg gac gag ccg tcc gac ccg 96
Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
20 25 30

atg atg aag cgc ttc gag gag tgg atg gtg gag tac ggc cgc gtg tac 144
Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
35 40 45

aag gac aac gac gag aag atg cgc cgc ttc cag atc ttc aag aac aac 192

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Lys	Asp	Asn	Asp	Glu	Lys	Met	Arg	Arg	Phe	Gln	Ile	Phe	Lys	Asn	Asn		
50				55						60							
gtg	aac	cac	atc	gag	acc	tcc	aac	cgc	aac	gag	aac	tcc	tac	acc		240	
Val	Asn	His	Ile	Glu	Thr	Phe	Asn	Ser	Arg	Asn	Glu	Asn	Ser	Tyr	Thr		
65				70					75				80				
ctc	ggc	atc	aac	cag	tcc	acc	gac	atg	acc	aac	aac	gag	tcc	atc	gcc		288
Leu	Gly	Ile	Asn	Gln	Phe	Thr	Asp	Met	Thr	Asn	Asn	Glu	Phe	Ile	Ala		
									85		90		95				
cag	tac	acc	ggc	ggc	atc	tcc	cgc	ccg	ctc	aac	atc	gag	cgc	gag	ccg		336
Gln	Tyr	Thr	Gly	Gly	Ile	Ser	Arg	Pro	Leu	Asn	Ile	Glu	Arg	Glu	Pro		
								100		105		110					
gtg	gtg	tcc	tcc	gac	gac	gtg	gac	atc	tcc	gcc	gtg	ccg	cag	tcc	atc		384
Val	Val	Ser	Phe	Asp	Asp	Val	Asp	Ile	Ser	Ala	Val	Pro	Gln	Ser	Ile		
						115		120				125					
gac	tgg	cgc	gac	tac	ggc	gcc	gtg	acc	tcc	gtg	aag	aac	cag	aac	ccg		432
Asp	Trp	Arg	Asp	Tyr	Gly	Ala	Val	Thr	Ser	Val	Lys	Asn	Gln	Asn	Pro		
						130		135			140						
tgc	ggc	gcc	tgc	tgg	gcc	tcc	gcc	atc	gcc	acc	gtg	gag	tcc	atc			480
Cys	Gly	Ala	Cys	Trp	Ala	Phe	Ala	Ala	Ile	Ala	Thr	Val	Glu	Ser	Ile		
						145		150			155			160			
tac	aag	atc	aag	aag	ggc	atc	ctc	gag	ccg	ctc	tcc	gag	cag	cag	gtg		528
Tyr	Lys	Ile	Lys	Lys	Gly	Ile	Leu	Glu	Pro	Leu	Ser	Glu	Gln	Gln	Val		
						165			170				175				
ctc	gac	tgc	gcc	aag	ggc	tac	ggc	tgc	aag	ggc	ggc	tgg	gag	tcc	cgc		576
Leu	Asp	Cys	Ala	Lys	Gly	Tyr	Gly	Cys	Lys	Gly	Gly	Trp	Glu	Phe	Arg		
						180		185				190					
gcc	ttc	gag	ttc	atc	atc	tcc	aac	aag	ggc	gtg	gcc	tcc	ggc	gcc	atc		624
Ala	Phe	Glu	Phe	Ile	Ile	Ser	Asn	Lys	Gly	Val	Ala	Ser	Gly	Ala	Ile		
						195		200			205						
tac	ccg	tac	aag	gcc	gcc	aag	ggc	acc	tgc	aag	acc	gac	ggc	gtg	ccg		672
Tyr	Pro	Tyr	Lys	Ala	Ala	Lys	Gly	Thr	Cys	Lys	Thr	Asp	Gly	Val	Pro		
						210		215			220						
aac	tcc	gcc	tac	atc	acc	ggc	tac	gcc	cgc	gtg	ccg	cgc	aac	aac	gag		720
Asn	Ser	Ala	Tyr	Ile	Thr	Gly	Tyr	Ala	Arg	Val	Pro	Arg	Asn	Asn	Glu		
						225		230			235			240			
tcc	tcc	atg	atg	tac	gcc	gtg	tcc	aag	cag	ccg	atc	acc	gtg	gcc	gtg		768
Ser	Ser	Met	Met	Tyr	Ala	Val	Ser	Lys	Gln	Pro	Ile	Thr	Val	Ala	Val		
						245			250				255				
gac	gcc	aac	gcc	aac	ttc	cag	tac	tac	aag	tcc	ggc	gtg	ttc	aac	ggc		816
Asp	Ala	Asn	Ala	Asn	Phe	Gln	Tyr	Tyr	Lys	Ser	Gly	Val	Phe	Asn	Gly		
						260			265			270					
ccg	tgc	ggc	acc	tcc	ctc	aac	cac	gcc	gtg	acc	gcc	atc	ggc	tac	ggc		864
Pro	Cys	Gly	Thr	Ser	Leu	Asn	His	Ala	Val	Thr	Ala	Ile	Gly	Tyr	Gly		
						275			280			285					
cag	gac	tcc	atc	atc	tac	ccg	aag	aag	tgg	ggc	gcc	aag	tgg	ggc	gag		912
Gln	Asp	Ser	Ile	Ile	Tyr	Pro	Lys	Lys	Trp	Gly	Ala	Lys	Trp	Gly	Glu		
						290			295			300					

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gcc ggc tac atc cgc atg gcc cgc gac gtg tcc tcc tcc ggc atc Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile 305 310 315 320	960
tgc ggc atc gcc atc gac ccg ctc tac ccg acc ctc gag gag tag Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu 325 330	1005
<210> 70	
<211> 334	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Synthetic Construct	
<400> 70	
Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val 1 5 10 15	
Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro 20 25 30	
Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr 35 40 45	
Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn 50 55 60	
Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr 65 70 75 80	
Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala 85 90 95	
Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro 100 105 110	
Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile 115 120 125	
Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro 130 135 140	
Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile 145 150 155 160	
Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val 165 170 175	

60110USPCT1 Corrected SEQ LIST 2-2007.txt
Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
180 185 190

Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
195 200 205

Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
210 215 220

Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
225 230 235 240

Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
245 250 255

Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
260 265 270

Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
275 280 285

Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
290 295 300

Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
305 310 315 320

Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
325 330

<210> 71
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Bromealin signal sequence

<400> 71
atggcctgga aggtgcaggt ggtgttcctc ttcctttcc tctgcgtgat gtgggcctcc 60
ccgtccgccc cctccgcc 78

<210> 72
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Bromealin signal peptide

<400> 72

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala
20 25

<210> 73
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11000

<400> 73
atggcctgga aggtgcaggt ggtgttcctc ttcctttcc tctgcgtgat gtgggcctcc 60
ccgtccgcgg cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg 120
atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgcg cttccagatc 180
ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctcctacacc 240
ctcggcatca accagttcac cgacatgacc aacaacgagt tcatacgccca gtacaccggc 300
ggcatctccc gcccgtcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360
atctccgcgg tgccgcagtc catcgactgg cgcgactacg ggcgcgtgac ctccgtgaag 420
aaccagaacc cgtgcggcgc ctgctggcc ttcgcccaca tcgcccaccgt ggagtccatc 480
tacaagatca agaaggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540
aagggtacg gctgcaaggc cggctggag ttccgcgcct tcgagttcat catctccaac 600
aagggtgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc 660
gacggcgtgc cgaactccgc ctacatcacc ggctacgccc gcgtgcgcg caacaacgag 720
tcctccatga tgtacgcccgt gtccaaagcag ccgatcaccg tggccgtgga cgccaaacgcc 780
aacttccagt actacaagtc cggcgtttc aacggccgt gcggcacctc cctcaaccac 840
gccgtgaccg ccatcggtcta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900
aagtggggcg aggccggcta catccgcattt gcccgcgacg tgtcctcctc ctccggcatc 960
tgccggcatcg ccatcgaccc gctctacccg accctcgagg aggtgttcgc cgaggccatc 1020
gccgccaact ccaccctcggt ggccgagtag 1050

<210> 74
<211> 1067
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11589

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 74	tggcctggaa ggtgcaggtg gtgttcctct tcctttccct ctgcgtgatg tgggcctccc	60
	cgtccgcgc ctccgcctcc tcctcctcct tcgccgactc caaccgatc cgcccggtga	120
	ccgaccgcgc cgccctccacc gacgagccgt ccgaccgat gatgaagcgc ttgcaggagt	180
	ggatggtggaa gtacggccgc gtgtacaagg acaacgacga gaagatgcgc cgcttccaga	240
	tcttcaagaa caacgtgaac cacatcgaga cttcaactc ccgcaacgag aactcctaca	300
	ccctcggcat caaccagttc accgacatga ccaacaacga gttcatcgcc cagtacaccg	360
	gcggcatctc ccgccccctc aacatcgagc gcgagccgt ggtgtccttc gacgacgtgg	420
	acatctccgc cgtgccgcag tccatcgact ggccgacta cggcccggt acctccgtga	480
	agaaccagaa cccgtgcggc gcctgctggg cttcgccgc catcgccacc gtggagtcca	540
	tctacaagat caagaagggc atcctcgagc cgctctccga gcagcaggtg ctcgactgcg	600
	ccaagggcta cggctgcaag ggcggctggg agttccgcgc ttgcagttc atcatctcca	660
	acaagggcgt ggcctccggc gccatctacc cgtacaaggc cgccaagggc acctgcaaga	720
	ccgacggcgt gccgaactcc gcctacatca cggctacgc ccgcgtgccc cgcaacaacg	780
	agtccctccat gatgtacgcc gtgtccaagc agccgatcac cgtggccgtg gacgccaacg	840
	ccaacttcca gtactacaag tccggcgtgt tcaacggccc gtgcggcacc tccctcaacc	900
	acgccgtac cccatcgac tacggccagg actccatcat ctacccgaag aagtggggcg	960
	ccaagtgggg cgaggccggc tacatccgca tggcccgca cgtgtcctcc tcctccggca	1020
	tctgcggcat cccatcgac ccgctctacc cgaccctcgaa ggatgt	1067

<210> 75
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11587 Sequence

<400> 75	atggcctggaa aggtgcaggt ggtgttcctc ttccctttcc tctgcgtgat gtgggcctcc	60
	ccgtccgcgc cttccgcggaa cgagccgtcc gacccatgaa tgaagcgctt cgaggagtgg	120
	atggtggtt acggccgcgt gtacaaggac aacgacgaga agatgcgcgc cttccatgtc	180
	ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctcctacacc	240
	ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc	300
	ggcatctccc gcccgtcaa catcgagcgc gagccgtgg tgtccttcga cgacgtggac	360
	atctccgcgc tgccgcagtc catcgactgg cgccactacg ggcgcgtgac ctccgtgaag	420
	aaccagaacc cgtgcggcgc ctgctggcc ttgcggcca tcgcccaccgt ggagtccatc	480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tacaagatca agaaggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgc	540
aaggctacg gctgcaaggg cggctggag ttccgcgcct tcgagttcat catctccaac	600
aaggcggtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc	660
gacggcgtgc cgaactccgc ctacatcacc ggctacgccc gcgtgcgcg caacaacgag	720
tcctccatga tgtacgccgt gtccaaagcag ccgatcaccg tggccgtgga cgccaaacgcc	780
aacctccagt actacaagtc cggcgttgc aacggccgt gcggcacctc cctcaaccac	840
gccgtgaccg ccatcggtta cggccaggac tccatcatct acccgaagaa gtggggcgcc	900
aagtggggcg aggccggcta catccgcatg gcccgacg tgcctcctc ctccggcatc	960
tgccgtatcg ccatcgaccc gctctacccg accctcgagg agtccgagaa ggacgagctg	1020
tag	1023

<210> 76
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN12169 Sequence

<400> 76	
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gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggt ggagtacggc	120
cgcgtgtaca aggacaacga cgagaagatg cgccgcttcc agatcttcaa gaacaacgtg	180
aaccacatcg agaccttcaa ctcccgcaac gagaactcct acaccctcg catcaaccag	240
ttcacccgaca tgaccaacaa cgagttcatc gcccagtaca cccggccat ctcccgcccc	300
ctcaacatcg agcgcgagcc ggtgggtgtcc ttgcacgacg tggacatctc cgccgtgccc	360
cagtccatcg actggcgcga ctacggcgcc gtgacctccg tgaagaacca gaaccgtgc	420
ggcgcctgct gggcattcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag	480
ggcatcctcg agccgctctc cgagcagcag gtgctcgact ggcaccaaggg ctacggctgc	540
aaggcggtgt gggagttccg cgcattcgag ttcatcatct ccaacaaggg cgtggcctcc	600
ggcgccatct acccgtaaaa ggcgcacaa ggcacctgca agaccgacgg cgtgccgaac	660
tccgcctaca tcaccggcta cgcccggtg ccgcgcaca acgagtcctc catgtatgtac	720
gccgtgtcca agcagccat caccgtggcc gtggacgcca acgccaactt ccagtactac	780
aagtccggcg tttcaacgg cccgtcgcc acctccctca accacgcccgt gaccgcccattc	840
ggctacggcc aggactccat catctacccg aagaagtgg ggcaccaagtg gggcgaggcc	900
ggctacatcc gcatggcccg cgacgtgtcc tcctcctccg gcatctgcgg catgcacatc	960
gaccggctct acccgaccct cgaggatag	990

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<210> 77
<211> 1170
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN12575 Sequence

<400> 77
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gacgcgtccacgttccgcccgcgcggcgcgcgcgcgcgcgcgcgcgc
gcggcggaca cgctcagcat gcggaccaggcgcgcgcgcgcgcgcgc
caggc
gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatgg
cgctgtaca aggacaacga cgagaagatgcgcgcgcgcgcgcgcgc
aaccacatcg agacattcaa ctcccgcaac gagaactcct acaccctcgg
ttcaccgaca tgaccaacaa cgagttcatc gccagtaca ccggcggcat
ctcaacatcg agcgcgagcc ggtggtgtcc ttcgacgacg tggacatctc
cagtccatcg actggcgca ctacggcgcc gtgacctccgc tgaagaacca
ggcgcctgct gggccttcgc cgccatcgcc accgtggagt ccatctacaa
ggcatcctcg agccgctctc cgagcagcag gtgctcgact ggcgcctg
aaggcggtcttcccg cgccatcgag ttcatcatct ccaacaaggcgtgc
ggcgccatct acccgtaaaa ggccgccaag ggcacctgca agaccgacgg
tccgcctaca tcacccggcta cgcccgctgtcccgcaaca acgagtcctc
gccgtgtcca agcagccat caccgtggcc gtggacgcca acgccaactt
aagtccggcg tttcaacgg cccgtcgcc acctccctca accacgcccgt
ggctacggcc aggactccat catctacccg aagaagtgg ggcgcctcc
ggctacatcc gcatggcccg cgacgtgtcc tcctcctccgc gcatctgcgg
gaccggctct acccgaccct cgaggagtag
1170

<210> 78
<211> 1068
<212> DNA
<213> Artificial Sequence

<220>
<223> psm270 Sequence

<400> 78
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gtggccctcc 60

60110USPCT1 Corrected SEQ LIST 2-2007.txt

ccgtccgccc	cctccgcctc	ctcctcctcc	ttcgccact	ccaacccgat	ccgcccggtg	120
accgaccgcg	ccgcctccac	cgacgagccg	tccgaccga	tgatgaagcg	cttcgaggag	180
tggatggtgg	agtacggccg	cgtgtacaag	gacaacgacg	agaagatgcg	ccgcttccag	240
atcttcaaga	acaacgtgaa	ccacatcgag	accttcaact	cccgcaacga	gaactcctac	300
accctcggca	tcaaccagtt	caccgacatg	accaacaacg	agttcatcgc	ccagtacacc	360
ggcggcatct	cccgcccgt	caacatcgag	cgcgagccgg	tggtgtcctt	cgacgacgtg	420
gacatctccg	ccgtgcccga	gtccatcgac	tggcgcgact	acggcgccgt	gacctccgtg	480
aagaaccaga	acccgtgcgg	cgcctgctgg	gccttcgccc	ccatcgccac	cgtggagtcc	540
atctacaaga	tcaagaaggg	catcctcgag	ccgctctccg	agcagcaggt	gctcgactgc	600
gccaagggct	acggctgcaa	ggcggctgg	gagttccgcg	cttcgagtt	catcatctcc	660
aacaaggcg	tggcctccgg	cgcctatctac	ccgtacaagg	ccgccaaggg	cacctgcaag	720
accgacggcg	tgccgaactc	cgcctacatc	accggctacg	ccgcgtgcc	gwgcaacaac	780
gagtcctcca	tgatgtacgc	cgtgtccaag	cagccatca	ccgtggccgt	ggacgccaac	840
gccaacttcc	agtactaca	gtccggcgtg	ttcaacggcc	cgtgcggcac	ctccctcaac	900
cacgcccgtga	ccgccccatcg	ctacggccag	gactccatca	tctacccgaa	gaagtggggc	960
gccaagtgg	gcgaggccgg	ctacatccgc	atggcccgcg	acgtgtcctc	ctcctccggc	1020
atctgcggca	tcgccccatcg	cccgctctac	ccgaccctcg	aggagtag		1068

<210> 79
 <211> 1497
 <212> DNA
 <213> Trichoderma reesei

<220>
 <221> CDS
 <222> (1)..(1497)
 <223> Trichoderma reesei cellobiohydrolase I

<400> 79	
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Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr	
1 5 10 15	
tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc	96
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser	
20 25 30	
gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc	144
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser	
35 40 45	
acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac	192
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp	
50 55 60	

60110USPCT1 Corrected SEQ LIST 2-2007.txt

aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala 65 70 75 80	240
tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt Ser Thr Tyr Gly Val Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe 85 90 95	288
gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met 100 105 110	336
gcu agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe 115 120 125	384
tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala 130 135 140	432
ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro 145 150 155 160	480
acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln 165 170 175	528
tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly 180 185 190	576
tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly 195 200 205	624
agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu 210 215 220	672
gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu 225 230 235 240	720
ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr 245 250 255	768
tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr 260 265 270	816
agc ttc tac ggc cct ggc tct agc ttt acc ctc gat acc acc aag aaa Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys 275 280 285	864
ttg acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac cga tac Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr 290 295 300	912
tat gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag ctt ggt Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly 305 310 315 320	960

60110USPCT1 Corrected SEQ LIST 2-2007.txt

agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag	1008
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu	
325 330 335	
gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg act cag	1056
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln	
340 345 350	
ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg	1104
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp	
355 360 365	
gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca	1152
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr	
370 375 380	
aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc	1200
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr	
385 390 395 400	
agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag	1248
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys	
405 410 415	
gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac	1296
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn	
420 425 430	
cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc	1344
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr	
435 440 445	
acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag	1392
Thr Arg Arg Pro Ala Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln	
450 455 460	
tct cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc acg gtc	1440
Ser His Tyr Gly Gln Cys Gly Ile Gly Tyr Ser Gly Pro Thr Val	
465 470 475 480	
tgc gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac tct cag	1488
Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln	
485 490 495	
tgc ctg taa	1497
Cys Leu	

<210> 80
<211> 498
<212> PRT
<213> Trichoderma reesei

<400> 80

Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
1 5 10 15

Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

60110USPCT1 Corrected SEQ LIST 2-2007.txt

val val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
35 40 45

Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
50 55 60

Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
65 70 75 80

Ser Thr Tyr Gly val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
85 90 95

val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
100 105 110

Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
115 120 125

Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
130 135 140

Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
145 150 155 160

Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
165 170 175

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
180 185 190

Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
195 200 205

Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
210 215 220

Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
225 230 235 240

Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
245 250 255

Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
260 265 270

Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
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60110USPCT1 Corrected SEQ LIST 2-2007.txt
280 285

Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
290 295 300

Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
305 310 315 320

Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
325 330 335

Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
340 345 350

Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
355 360 365

Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
370 375 380

Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
385 390 395 400

Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
405 410 415

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
420 425 430

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
435 440 445

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
450 455 460

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
465 470 475 480

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
485 490 495

Cys Leu

<210> 81
<211> 1365
<212> DNA
<213> Trichoderma reesei

60110USPCT1 Corrected SEQ LIST 2-2007.txt

60110USPCT1 Corrected SEQ LIST 2-2007.txt

att gag cct gac tct ctt gcc aac ctg gtg acc aac ctc ggt act cca Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro 225 230 235 240	720
aag tgt gcc aat gct cag tca gcc tac ctt gag tgc atc aac tac gcc Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala 245 250 255	768
gtc aca cag ctg aac ctt cca aat gtt gcg atg tat ttg gac gct ggc Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly 260 265 270	816
cat gca gga tgg ctt ggc tgg ccg gca aac caa gac ccg gcc gct cag His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln 275 280 285	864
cta ttt gca aat gtt tac aag aat gca tcg tct ccg aga gct ctt cgc Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg 290 295 300	912
gga ttg gca acc aat gtc gcc aac tac aac ggg tgg aac att acc agc Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser 305 310 315 320	960
ccc cca tcg tac acg caa ggc aac gct gtc tac aac gag aag ctg tac Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr 325 330 335	1008
atc cac gct att gga cct ctt gcc aat cac ggc tgg tcc aac gcc Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala 340 345 350	1056
ttc ttc atc act gat caa ggt cga tcg gga aag cag cct acc gga cag Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln 355 360 365	1104
caa cag tgg gga gac tgg tgc aat gtg atc ggc acc gga ttt ggt att Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile 370 375 380	1152
cgc cca tcc gca aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp 385 390 395 400	1200
gtc aag cca ggc ggc gag tgt gac ggc acc agc gac agc agt gcg cca Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro 405 410 415	1248
cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg caa ccg gcg cct Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro 420 425 430	1296
caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn 435 440 445	1344
gca aac cca tcg ttc ctg tag Ala Asn Pro Ser Phe Leu 450	1365

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<211> 454

<212> PRT

<213> Trichoderma reesei

<400> 82

Met Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly Gln
1 5 10 15

Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
20 25 30

Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
35 40 45

Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
50 55 60

Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
65 70 75 80

Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser
85 90 95

Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala
100 105 110

Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala
115 120 125

Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp
130 135 140

Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg
145 150 155 160

Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr
165 170 175

Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr
180 185 190

Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr
195 200 205

Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val
210 215 220

Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro
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60110USPCT1 Corrected SEQ LIST 2-2007.txt
230 235 240

Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala
245 250 255

val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
260 265 270

His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln
275 280 285

Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg
290 295 300

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser
305 310 315 320

Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
325 330 335

Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
340 345 350

Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
355 360 365

Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
370 375 380

Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
385 390 395 400

Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
405 410 415

Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
420 425 430

Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
435 440 445

Ala Asn Pro Ser Phe Leu
450

<210> 83
<211> 1317
<212> DNA
<213> Trichoderma reesei

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>
 <221> CDS
 <222> (1)..(1317)
 <223> Trichoderma reesei endoglucanase I

<400> 83

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Met	Gln	Gln	Pro	Gly	Thr	Ser	Thr	Pro	Glu	Val	His	Pro	Lys	Leu	Thr		
1				5					10					15			
acc	tac	aag	tgc	aca	aag	tcc	ggg	ggg	tgc	gtg	gcc	cag	gac	acc	tcg		96
Thr	Tyr	Lys	Cys	Thr	Lys	Ser	Gly	Gly	Cys	Val	Ala	Gln	Asp	Thr	Ser		
				20				25					30				
gtg	gtc	ctt	gac	tgg	aac	tac	cgc	tgg	atg	cac	gac	gca	aac	tac	aac		144
Val	Val	Leu	Asp	Trp	Asn	Tyr	Arg	Trp	Met	His	Asp	Ala	Asn	Tyr	Asn		
				35			40				45						
tcg	tgc	acc	gtc	aac	ggc	ggc	gtc	aac	acc	acg	ctc	tgc	cct	gac	gag		192
Ser	Cys	Thr	Val	Asn	Gly	Gly	Val	Asn	Thr	Thr	Leu	Cys	Pro	Asp	Glu		
				50			55				60						
gcg	acc	tgt	ggc	aag	aac	tgc	ttc	atc	gag	ggc	gtc	gac	tac	gcc	gcc		240
Ala	Thr	Cys	Gly	Lys	Asn	Cys	Phe	Ile	Glu	Gly	Val	Asp	Tyr	Ala	Ala		
				65			70			75				80			
tcg	ggc	gtc	acg	acc	tcg	ggc	agc	agc	ctc	acc	atg	aac	cag	tac	atg		288
Ser	Gly	Val	Thr	Thr	Ser	Gly	Ser	Ser	Leu	Thr	Met	Asn	Gln	Tyr	Met		
				85				90					95				
ccc	agc	agc	tct	ggc	ggc	tac	agc	agc	gtc	tct	cct	cg	ctg	tat	ctc		336
Pro	Ser	Ser	Ser	Gly	Gly	Tyr	Ser	Ser	Val	Ser	Pro	Arg	Leu	Tyr	Leu		
				100				105					110				
ctg	gac	tct	gac	ggt	gag	tac	gtg	atg	ctg	aag	ctc	aac	ggc	cag	gag		384
Leu	Asp	Ser	Asp	Gly	Glu	Tyr	Val	Met	Leu	Lys	Leu	Asn	Gly	Gln	Glu		
				115			120					125					
ctg	agc	ttc	gac	gtc	gac	ctc	tct	gct	ctg	ccg	tgt	gga	gag	aac	ggc		432
Leu	Ser	Phe	Asp	Val	Asp	Leu	Ser	Ala	Leu	Pro	Cys	Gly	Glu	Asn	Gly		
				130			135			140							
tcg	ctc	tac	ctg	tct	cag	atg	gac	gag	aac	ggg	ggc	gcc	aac	cag	tat		480
Ser	Leu	Tyr	Leu	Ser	Gln	Met	Asp	Glu	Asn	Gly	Gly	Ala	Asn	Gln	Tyr		
				145			150			155				160			
aac	acg	gcc	ggt	gcc	aac	tac	ggg	agc	ggc	tac	tgc	gat	gct	cag	tgc		528
Asn	Thr	Ala	Gly	Ala	Asn	Tyr	Gly	Ser	Gly	Tyr	Cys	Asp	Ala	Gln	Cys		
				165				170					175				
ccc	gtc	cag	aca	tgg	agg	aac	ggc	acc	ctc	aac	act	agc	cac	cag	ggc		576
Pro	Val	Gln	Thr	Trp	Arg	Asn	Gly	Thr	Leu	Asn	Thr	Ser	His	Gln	Gly		
				180				185					190				
ttc	tgc	tgc	aac	gag	atg	gat	atc	ctg	gag	ggc	aac	tcg	agg	gcg	aat		624
Phe	Cys	Cys	Asn	Glu	Met	Asp	Ile	Leu	Glu	Gly	Asn	Ser	Arg	Ala	Asn		
				195				200					205				
gcc	ttg	acc	cct	cac	tct	tgc	acg	gcc	acg	gcc	tgc	gac	tct	gcc	ggt		672
Ala	Leu	Thr	Pro	His	Ser	Cys	Thr	Ala	Thr	Ala	Cys	Asp	Ser	Ala	Gly		
				210			215				220						

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro 225 230 235 240	720
gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe 245 250 255	768
aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg 260 265 270	816
aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly 275 280 285	864
gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala 290 295 300	912
acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile 305 310 315 320	960
tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala 325 330 335	1008
ggc ccc tgc agc agc acc gag ggc aac cca tcc aac acc ctg gcc aac Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn 340 345 350	1056
aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile 355 360 365	1104
ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Ala Ser Ser 370 375 380	1152
acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg Thr Thr Phe Ser Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro 385 390 395 400	1200
agc tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg tac agc Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Ile Gly Tyr Ser 405 410 415	1248
ggg tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc aac gac Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp 420 425 430	1296
tac tac tcg caa tgc ctt tag Tyr Tyr Ser Gln Cys Leu 435	1317

<210> 84
<211> 438
<212> PRT
<213> Trichoderma reesei

<400> 84

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
1 5 10 15

Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
20 25 30

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
35 40 45

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
50 55 60

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
65 70 75 80

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
85 90 95

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
100 105 110

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
115 120 125

Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
130 135 140

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
145 150 155 160

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
165 170 175

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
180 185 190

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
195 200 205

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
210 215 220

Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
225 230 235 240

Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
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245 60110USPCT1 Corrected SEQ LIST 2-2007.txt
250
255

Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
260 265 270

Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
275 280 285

Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
290 295 300

Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
305 310 315 320

Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
325 330 335

Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
340 345 350

Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
355 360 365

Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
370 375 380

Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
385 390 395 400

Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
405 410 415

Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
420 425 430

Tyr Tyr Ser Gln Cys Leu
435

<210> 85
<211> 954
<212> DNA
<213> Artificial sequence

<220>
<223> 6GP1

<220>
<221> CDS
<222> (1)..(954)

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<223> 6GP1

<400> 85

atg ggc gtg gac ccg ttc gag cgc aac aag atc ctc ggc cgc ggc atc Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile 1 5 10 15	48
aac atc ggc aac gcc ctg gag gcc ccg aac gag ggc gac tgg ggc gtg Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val 20 25 30	96
gtg atc aag gac gag ttc ttc gac atc atc aag gag gcc ggc ttc tcc Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser 35 40 45	144
cac gtg cgc atc ccg atc cgc tgg tcc acc cac gcc tac gcc ttc ccg His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro 50 55 60	192
ccg tac aag atc atg gac cgc ttc ttc aag cgc gtg gac gag gtg atc Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile 65 70 75 80	240
aac ggc gcc ctc aag cgc ggc ctc gcc gtg gcc atc aac atc cac cac Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His 85 90 95	288
tac gag gag ctc atg aac gac ccg gag gag cac aag gag cgc ttc ctc Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu 100 105 110	336
gcc ctc tgg aag cag atc gcc gac cgc tac aag gac tac ccg gag acc Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr 115 120 125	384
ctc ttc ttc gag atc ctc aac gag ccg cac ggc aac ctc acc ccg gag Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu 130 135 140	432
aag tgg aac gag ctg ctc gag gag gcc ctc aag gtg atc cgc tcc atc Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile 145 150 155 160	480
gac aag aag cac acc atc atc att ggc acc gca gag tgg gga ggc atc Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile 165 170 175	528
tcc gcc ctc gag aag ctc tcc gtg ccg aag tgg gag aag aat tcc atc Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile 180 185 190	576
gtg acc atc cac tac tac aac ccg ttc gag ttc acg cac cag ggc gcc Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala 195 200 205	624
gag tgg gtg gag ggc tcc gag aag tgg ctt ggc cgc aag tgg ggc tcc Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser 210 215 220	672
ccg gac gac cag aag cac ctc atc gag gag ttc aac ttc atc gag gag Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu 225 230 235 240	720

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgg tcc aag aag aac aag cgc ccg atc tac atc ggc gag ttt ggc gcc Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala 245 250 255	768
tac cgc aag gcc gac ctc gag tcc cgc atc aag tgg acc tcc ttc gtg Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val 260 265 270	816
gtg cgt gag atg gag aag cgc cgc tgg tcc tgg gcc tac tgg gag ttc Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe 275 280 285	864
tgc tcc ggc ttc ggc gtg tac gac acc ctc cgc aag acc tgg aac aag Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys 290 295 300	912
gac ctc ctc gag gcc ctc atc ggc ggc gac tcc atc gag tag Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu 305 310 315	954

<210> 86
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 86

Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile
1 5 10 15

Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
20 25 30

Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
35 40 45

His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
50 55 60

Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
65 70 75 80

Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
85 90 95

Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
100 105 110

Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
115 120 125

60110USPCT1 Corrected SEQ LIST 2-2007.txt
Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
130 135 140

Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
145 150 155 160

Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
165 170 175

Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
180 185 190

Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
195 200 205

Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
210 215 220

Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
225 230 235 240

Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
245 250 255

Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
260 265 270

Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
275 280 285

Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
290 295 300

Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
305 310 315

<210> 87
<211> 1248
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (1)..(1248)
<223> Barley AmyI amylase

<400> 87
atg gca cac caa gtc ctc ttt cag ggg ttc aac tgg gag tcg tgg aag 48
Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
1 5 10 15

60110USPCT1 Corrected SEQ LIST 2-2007.txt

cag	agc	ggc	ggg	tgg	tac	aac	atg	atg	atg	ggc	aag	gtc	gac	gac	atc	96
Gln	Ser	Gly	Gly	Trp	Tyr	Asn	Met	Met	Met	Gly	Lys	Val	Asp	Asp	Ile	
20							25					30				
gcc	gct	gcc	gga	gtc	acc	cac	gtc	tgg	ctg	cca	ccg	ccg	tcg	cac	tcc	144
Ala	Ala	Ala	Gly	Val	Thr	His	Val	Trp	Leu	Pro	Pro	Pro	Ser	His	Ser	
35							40					45				
gtc	tcc	aac	gaa	ggt	tac	atg	cct	ggt	cg	ctg	tac	gac	atc	gac	gcg	192
Val	Ser	Asn	Glu	Gly	Tyr	Met	Pro	Gly	Arg	Leu	Tyr	Asp	Ile	Asp	Ala	
50						55				60						
tcc	aag	tac	ggc	aac	gcf	gcf	gag	ctc	aag	tcg	ctc	atc	ggc	gcf	ctc	240
Ser	Lys	Tyr	Gly	Asn	Ala	Ala	Glu	Leu	Lys	Ser	Leu	Ile	Gly	Ala	Leu	
65						70				75			80			
cac	ggc	aag	ggc	gtg	cag	gcc	atc	gcc	gac	atc	gtc	atc	aac	cac	cgc	288
His	Gly	Lys	Gly	Val	Gln	Ala	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	
85							90						95			
tgc	gcc	gac	tac	aag	gat	agc	cgc	ggc	atc	tac	tgc	atc	ttc	gag	ggc	336
Cys	Ala	Asp	Tyr	Lys	Asp	Ser	Arg	Gly	Ile	Tyr	Cys	Ile	Phe	Glu	Gly	
100							105						110			
ggc	acc	tcc	gac	ggc	cgc	ctc	gac	tgg	ggc	ccc	cac	atg	atc	tgt	cgc	384
Gly	Thr	Ser	Asp	Gly	Arg	Leu	Asp	Trp	Gly	Pro	His	Met	Ile	Cys	Arg	
115						120						125				
gac	gac	acc	aaa	tac	tcc	gat	ggc	acc	gca	aac	ctc	gac	acc	gga	gcc	432
Asp	Asp	Thr	Lys	Tyr	Ser	Asp	Gly	Thr	Ala	Asn	Leu	Asp	Thr	Gly	Ala	
130						135						140				
gac	tcc	gcc	gcc	gcf	ccc	gac	atc	gac	cac	ctc	aac	gac	cg	gtc	cag	480
Asp	Phe	Ala	Ala	Ala	Pro	Asp	Ile	Asp	His	Leu	Asn	Asp	Arg	Val	Gln	
145						150				155					160	
cgc	gag	ctc	aag	gag	tgg	ctc	ctc	tgg	ctc	aag	agc	gac	ctc	ggc	ttc	528
Arg	Glu	Leu	Lys	Glu	Trp	Leu	Leu	Trp	Leu	Lys	Ser	Asp	Leu	Gly	Phe	
165							170						175			
gac	gcf	tgg	cgc	ctt	gac	tcc	gcc	agg	ggc	tac	tcg	ccg	gag	atg	gcc	576
Asp	Ala	Trp	Arg	Leu	Asp	Phe	Ala	Arg	Gly	Tyr	Ser	Pro	Glu	Met	Ala	
180						185							190			
aag	gtg	tac	atc	gac	ggc	aca	tcc	ccg	agc	ctc	gcc	gtg	gcc	gag	gtg	624
Lys	Val	Tyr	Ile	Asp	Gly	Thr	Ser	Pro	Ser	Leu	Ala	Val	Ala	Glu	Val	
195						200						205				
tgg	gac	aat	atg	gcc	acc	ggc	ggc	gac	ggc	aag	ccc	aac	tac	gac	cag	672
Trp	Asp	Asn	Met	Ala	Thr	Gly	Gly	Asp	Gly	Lys	Pro	Asn	Tyr	Asp	Gln	
210						215					220					
gac	gcf	cac	cgg	cag	aat	ctg	gtg	aac	tgg	gtg	gac	aag	gtg	ggc	ggc	720
Asp	Ala	His	Arg	Gln	Asn	Leu	Val	Asn	Trp	Val	Asp	Lys	Val	Gly	Gly	
225						230				235					240	
gcf	gcc	tcg	gca	ggc	atg	gtg	tcc	gac	tcc	acg	acc	aaa	ggg	ata	ctg	768
Ala	Ala	Ser	Ala	Gly	Met	Val	Phe	Asp	Phe	Thr	Thr	Lys	Gly	Ile	Leu	
245						250							255			
aac	gct	gcc	gtg	gag	ggc	gag	ctg	tgg	agg	ctg	atc	gac	ccg	cag	ggg	816
Asn	Ala	Ala	Val	Glu	Gly	Glu	Leu	Trp	Arg	Leu	Ile	Asp	Pro	Gln	Gly	

60110USPCT1 Corrected SEQ LIST 2-2007.txt

260

265

270

aag	gcc	ccc	gac	gtg	atg	gga	tgg	tgg	ccg	gcc	aag	gcc	gtc	acc	ttc		864
Lys	Ala	Pro	Gly	Val	Met	Gly	Trp	Trp	Pro	Ala	Lys	Ala	Val	Thr	Phe		
275					280						285						
gtc	gac	aac	cac	gat	aca	ggc	tcc	acg	cag	gcc	atg	tgg	cca	ttc	ccc		912
Val	Asp	Asn	His	Asp	Thr	Gly	Ser	Thr	Gln	Ala	Met	Trp	Pro	Phe	Pro		
290					295						300						
tcc	gac	aag	gtc	atg	cag	ggc	tac	gcf	tac	atc	ctc	acc	cac	ccc	ggc		960
Ser	Asp	Lys	Val	Met	Gln	Gly	Tyr	Ala	Tyr	Ile	Leu	Thr	His	Pro	Gly		
305					310					315					320		
atc	cca	tgc	atc	ttc	tac	gac	cat	ttc	ttc	aac	tgg	ggg	ttt	aag	gac		1008
Ile	Pro	Cys	Ile	Phe	Tyr	Asp	His	Phe	Phe	Asn	Trp	Gly	Phe	Lys	Asp		
325					330									335			
cag	atc	gac	gac	ctg	gtg	gac	atc	agg	aag	cgc	aac	ggc	atc	acg	gac		1056
Gln	Ile	Ala	Ala	Leu	Val	Ala	Ile	Arg	Lys	Arg	Asn	Gly	Ile	Thr	Ala		
340					345									350			
acg	agc	gct	ctg	aag	atc	ctc	atg	cac	gaa	gga	gat	gcc	tac	gtc	gcc		1104
Thr	Ser	Ala	Leu	Lys	Ile	Leu	Met	His	Glu	Gly	Asp	Ala	Tyr	Val	Ala		
355					360						365						
gag	ata	gac	gac	aag	gtg	gtg	gtg	aag	atc	ggg	tcc	agg	tac	gac	gtc		1152
Glu	Ile	Asp	Gly	Lys	Val	Val	Val	Lys	Ile	Gly	Ser	Arg	Tyr	Asp	Val		
370					375						380						
ggg	gac	gtg	atc	ccg	gcc	ggg	ttc	gtg	acc	tcg	gca	cac	ggc	aac	gac		1200
Gly	Ala	Val	Ile	Pro	Ala	Gly	Phe	Val	Thr	Ser	Ala	His	Gly	Asn	Asp		
385					390					395					400		
tac	gcc	gtc	tgg	gag	aag	aac	ggt	gcc	gac	gca	aca	cta	caa	cg	agc		1248
Tyr	Ala	Val	Trp	Glu	Lys	Asn	Gly	Ala	Ala	Ala	Ala	Thr	Leu	Gln	Arg	Ser	
405								410						415			

<210> 88

<211> 416

<212> PRT

<213> Hordeum vulgare

<400> 88

Met	Ala	His	Gln	Val	Leu	Phe	Gln	Gly	Phe	Asn	Trp	Glu	Ser	Trp	Lys	
1				5				10				15				

Gln	Ser	Gly	Gly	Trp	Tyr	Asn	Met	Met	Met	Gly	Lys	Val	Asp	Asp	Ile	
20					25							30				

Ala	Ala	Ala	Gly	Val	Thr	His	Val	Trp	Leu	Pro	Pro	Pro	Ser	His	Ser	
35					40							45				

Val	Ser	Asn	Glu	Gly	Tyr	Met	Pro	Gly	Arg	Leu	Tyr	Asp	Ile	Asp	Ala	
50					55					60						

Ser	Lys	Tyr	Gly	Asn	Ala	Ala	Glu	Leu	Lys	Ser	Leu	Ile	Gly	Ala	Leu	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

65

60110USPCT1 Corrected SEQ LIST 2-2007.txt
70 75 80

His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
85 90 95

Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
100 105 110

Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
115 120 125

Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
130 135 140

Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln
145 150 155 160

Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe
165 170 175

Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala
180 185 190

Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val
195 200 205

Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln
210 215 220

Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly
225 230 235 240

Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu
245 250 255

Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly
260 265 270

Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe
275 280 285

Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro
290 295 300

Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly
305 310 315 320

60110USPCT1 Corrected SEQ LIST 2-2007.txt
Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp
325 330 335

Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala
340 345 350

Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala
355 360 365

Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val
370 375 380

Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
385 390 395 400

Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
405 410 415

<210> 89
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Trichoderma reesei β -Glucosidase 2

<220>
<221> CDS
<222> (1)..(1401)
<223> Trichoderma reesei β -Glucosidase 2

<400> 89
atg ttg ccc aag gac ttt cag tgg ggg ttc gcc acg gct gcc tac cag 48
Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
1 5 10 15

atc gag ggc gcc gtc gac cag gac ggc cgc ggc ccc agc atc tgg gac 96
Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
20 25 30

acg ttc tgc gcg cag ccc ggc aag atc gcc gac ggc tcg tcg ggc gtg 144
Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
35 40 45

acg gcg tgc gac tcg tac aac cgc acg gcc gag gac att gcg ctg ctg 192
Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
50 55 60

aag tcg ctc ggg gcc aag agc tac cgc ttc tcc atc tcg tgg tcg cgc 240
Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
65 70 75 80

atc atc ccc gag ggc ggc cgc ggc gat gcc gtc aac cag gcg ggc atc 288
Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
85 90 95

60110USPCT1 Corrected SEQ LIST 2-2007.txt															
gac	cac	tac	gtc	aag	ttc	gtc	gac	gac	ctg	ctc	gac	gcc	ggc	atc	acg
Asp	His	Tyr	Val	Lys	Phe	Val	Asp	Asp	Leu	Leu	Asp	Ala	Gly	Ile	Thr
100					105							110			
ccc	ttc	atc	acc	ctc	ttc	cac	tgg	gac	ctg	ccc	gag	ggc	ctg	cat	cag
Pro	Phe	Ile	Thr	Leu	Phe	His	Trp	Asp	Leu	Pro	Glu	Gly	Leu	His	Gln
115					120						125				
cgg	tac	ggg	ggg	ctg	ctg	aac	cgc	acc	gag	ttc	ccg	ctc	gac	ttt	gaa
Arg	Tyr	Gly	Gly	Leu	Leu	Asn	Arg	Thr	Glu	Phe	Pro	Leu	Asp	Phe	Glu
130				135						140					
aac	tac	gcc	cgc	gtc	atg	ttc	agg	gcg	ctg	ccc	aag	gtg	cgc	aac	tgg
Asn	Tyr	Ala	Arg	Val	Met	Phe	Arg	Ala	Leu	Pro	Lys	Val	Arg	Asn	Trp
145				150					155			160			
atc	acc	ttc	aac	gag	ccg	ctg	tgc	tcg	gcc	atc	ccg	ggc	tac	ggc	tcc
Ile	Thr	Phe	Asn	Glu	Pro	Leu	Cys	Ser	Ala	Ile	Pro	Gly	Tyr	Gly	Ser
165				170								175			
ggc	acc	ttc	gcc	ccc	ggc	cgg	cag	agc	acc	tcg	gag	ccg	tgg	acc	gtc
Gly	Thr	Phe	Ala	Pro	Gly	Arg	Gln	Ser	Thr	Ser	Glu	Pro	Trp	Thr	Val
180				185							190				
ggc	cac	aac	atc	ctc	gtc	gcc	cac	ggc	cgc	gcc	gtc	aag	gcg	tac	cgc
Gly	His	Asn	Ile	Leu	Val	Ala	His	Gly	Arg	Ala	Val	Lys	Ala	Tyr	Arg
195				200							205				
gac	gac	ttc	aag	ccc	gcc	agc	ggc	gac	ggc	cag	atc	gtc	atc	gtc	ctc
Asp	Asp	Phe	Lys	Pro	Ala	Ser	Gly	Asp	Gly	Gln	Ile	Gly	Ile	Val	Leu
210				215						220					
aac	ggc	gac	ttc	acc	tac	ccc	tgg	gac	gcc	gac	ccg	gcc	gac	aag	
Asn	Gly	Asp	Phe	Thr	Tyr	Pro	Trp	Asp	Ala	Ala	Asp	Pro	Ala	Asp	Lys
225				230						235				240	
gag	gcf	gcc	gag	cgg	cgc	ctc	gag	tcc	tcc	acg	gcc	tgg	tcc	gcf	gac
Glu	Ala	Ala	Glu	Arg	Arg	Leu	Glu	Phe	Phe	Thr	Ala	Trp	Phe	Ala	Asp
245				250								255			
ccc	atc	tac	ttg	ggc	gac	tac	ccg	gcf	tcg	atg	cgc	aag	cag	ctg	ggc
Pro	Ile	Tyr	Leu	Gly	Asp	Tyr	Pro	Ala	Ser	Met	Arg	Lys	Gln	Leu	Gly
260				265							270				
gac	cgg	ctg	ccg	acc	ttt	acg	ccc	gag	gag	cgc	gcc	ctc	gtc	cac	ggc
Asp	Arg	Leu	Pro	Thr	Phe	Thr	Pro	Glu	Glu	Arg	Ala	Leu	Val	His	Gly
275				280							285				
tcc	aac	gac	ttt	tac	ggc	atg	aac	cac	tac	acg	tcc	aac	tac	atc	cgc
Ser	Asn	Asp	Phe	Tyr	Gly	Met	Asn	His	Tyr	Thr	Ser	Asn	Tyr	Ile	Arg
290				295						300					
cac	cgc	agc	tcg	ccc	gcc	tcc	gcc	gac	gac	acc	gtc	ggc	aac	gtc	gac
His	Arg	Ser	Ser	Pro	Ala	Ser	Ala	Asp	Asp	Thr	Val	Gly	Asn	Val	Asp
305				310						315				320	
gtg	ctc	ttc	acc	aac	aag	cag	ggc	aac	tgc	atc	ggc	ccc	gag	acg	cag
Val	Leu	Phe	Thr	Asn	Lys	Gln	Gly	Asn	Cys	Ile	Gly	Pro	Glu	Thr	Gln
325				330							335				
tcc	ccc	tgg	ctg	cgc	ccc	tgt	gcc	ggc	ttc	cgc	gac	ttc	ctg	gtg	
Ser	Pro	Trp	Leu	Arg	Pro	Cys	Ala	Ala	Gly	Phe	Arg	Asp	Phe	Leu	Val
340				345							350				

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgg atc agc aag agg tac ggc tac ccg ccc atc tac gtg acg gag aac Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn 355 360 365	1104
ggc acg agc atc aag ggc gag agc gac ttg ccc aag gag aag att ctc Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu 370 375 380	1152
gaa gat gac ttc agg gtc aag tac tat aac gag tac atc cgt gcc atg Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met 385 390 395 400	1200
gtt acc gcc gtg gag ctg gac ggg gtc aac gtc aag ggg tac ttt gcc Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Glu Tyr Phe Ala 405 410 415	1248
tgg tcg ctc atg gac aac ttt gag tgg gcg gac ggc tac gtg acg agg Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg 420 425 430	1296
ttt ggg gtt acg tat gtg gat tat gag aat ggg cag aag cggttccc Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro 435 440 445	1344
aag aag agc gca aag agc ttg aag ccg ctg ttt gac gag ctg att gcg Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala 450 455 460	1392
gcg gcg tga Ala Ala 465	1401

<210> 90
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct
<400> 90

Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
1 5 10 15

Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
20 25 30

Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly val
35 40 45

Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
50 55 60

Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
65 70 75 80

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
85 90 95

Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
100 105 110

Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
115 120 125

Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
130 135 140

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
145 150 155 160

Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
165 170 175

Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
180 185 190

Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
195 200 205

Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
210 215 220

Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
225 230 235 240

Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
245 250 255

Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
260 265 270

Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
275 280 285

Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
290 295 300

His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
305 310 315 320

Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
325 330 335

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
340 345 350

Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
355 360 365

Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
370 375 380

Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385 390 395 400

Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
405 410 415

Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
420 425 430

Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
435 440 445

Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
450 455 460

Ala Ala
465

<210> 91
<211> 2103
<212> DNA
<213> Artificial sequence

<220>
<223> Trichoderma reesei β -Glucosidase D

<220>
<221> CDS
<222> (1)..(2103)
<223> Trichoderma reesei β -Glucosidase D

<400> 91
atg att ctc ggc tgt gaa agc aca ggt gtc atc tct gcc gtc aaa cac 48
Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
1 5 10 15

ttt gtc gcc aac gac cag gag cac gag cg_g cga gc_g gtc gac tgt ctc 96
Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
20 25 30

atc acc cag cg_g gct ctc cg_g gag gtc tat ctg cga ccc ttc cag atc 144
Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile

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35

40

45

gta	gcc	cga	gat	gca	agg	ccc	ggc	gca	ttg	atg	aca	tcc	tac	aac	aag		192
Val	Ala	Arg	Asp	Ala	Arg	Pro	Gly	Ala	Leu	Met	Thr	Ser	Tyr	Asn	Lys		
50				55					60								
gtc	aat	ggc	aag	cac	gtc	gct	gac	agc	gcc	gag	ttc	ctt	cag	ggc	att		240
Val	Asn	Gly	Lys	His	Val	Ala	Asp	Ser	Ala	Glu	Phe	Leu	Gln	Gly	Ile		
65				70				75				80					
ctc	cgg	act	gag	tgg	aat	tgg	gac	cct	ctc	att	gtc	agc	gac	tgg	tac		288
Leu	Arg	Thr	Glu	Trp	Asn	Trp	Asp	Pro	Leu	Ile	Val	Ser	Asp	Trp	Tyr		
				85				90			95						
ggc	acc	tac	acc	act	att	gat	gcc	atc	aaa	gcc	ggc	ctt	gat	ctc	gag		336
Gly	Thr	Tyr	Thr	Thr	Ile	Asp	Ala	Ile	Lys	Ala	Gly	Leu	Asp	Leu	Glu		
				100				105			110						
atg	ccg	ggc	gtt	tca	cga	tat	cgc	ggc	aaa	tac	atc	gag	tct	gct	ctg		384
Met	Pro	Gly	Val	Ser	Arg	Tyr	Arg	Gly	Lys	Tyr	Ile	Glu	Ser	Ala	Leu		
				115				120			125						
cag	gcc	cgt	ttg	ctg	aag	cag	tcc	act	atc	gat	gag	cgc	gct	cgc	cgc		432
Gln	Ala	Arg	Leu	Leu	Lys	Gln	Ser	Thr	Ile	Asp	Glu	Arg	Ala	Arg	Arg		
				130				135			140						
gtg	ctc	agg	ttc	gcc	cag	aag	gcc	agc	cat	ctc	aag	gtc	tcc	gag	gta		480
Val	Leu	Arg	Phe	Ala	Gln	Lys	Ala	Ser	His	Leu	Lys	Val	Ser	Glu	Val		
				145				150			155			160			
gag	caa	ggc	cgt	gac	ttc	cca	gag	gat	cgc	gtc	ctc	aac	cgt	cag	atc		528
Glu	Gln	Gly	Arg	Asp	Phe	Pro	Glu	Asp	Arg	Val	Leu	Asn	Arg	Gln	Ile		
				165				170			175						
tgc	ggc	agc	agc	att	gtc	cta	ctg	aag	aat	gag	aac	tcc	atc	tta	cct		576
Cys	Gly	Ser	Ser	Ile	Val	Leu	Leu	Lys	Asn	Glu	Asn	Ser	Ile	Leu	Pro		
				180				185			190						
ctc	ccc	aag	tcc	gtc	aag	aag	gtc	gcc	ctt	gtt	ggt	tcc	cac	gtg	cgt		624
Leu	Pro	Lys	Ser	Val	Lys	Lys	Val	Ala	Leu	Val	Gly	Ser	His	Val	Arg		
				195				200			205						
cta	ccg	gct	atc	tcg	gga	gga	ggc	agc	gcc	tct	ctt	gtc	cct	tac	tat		672
Leu	Pro	Ala	Ile	Ser	Gly	Gly	Ser	Ala	Ser	Leu	Val	Pro	Tyr	Tyr			
				210				215			220						
gcc	ata	tct	cta	tac	gat	gcc	gtc	tct	gag	gta	cta	gcc	ggt	gcc	acg		720
Ala	Ile	Ser	Leu	Tyr	Asp	Ala	Val	Ser	Glu	Val	Leu	Ala	Gly	Ala	Thr		
				225				230			235			240			
atc	acg	cac	gag	gtc	ggt	gcc	tat	gcc	cac	caa	atg	ctg	ccc	gtc	atc		768
Ile	Thr	His	Glu	Val	Gly	Ala	Tyr	Ala	His	Gln	Met	Leu	Pro	Val	Ile		
				245				250			255						
gac	gca	atg	atc	agc	aac	gcc	gta	atc	cac	ttc	tac	aac	gac	ccc	atc		816
Asp	Ala	Met	Ile	Ser	Asn	Ala	Val	Ile	His	Phe	Tyr	Asn	Asp	Pro	Ile		
				260				265			270						
gat	gtc	aaa	gac	aga	aag	ctc	ctt	ggc	agt	gag	aac	gta	tcg	tcg	aca		864
Asp	Val	Lys	Asp	Arg	Lys	Leu	Leu	Gly	Ser	Glu	Asn	Val	Ser	Ser	Thr		
				275				280			285						
tcg	ttc	cag	ctc	atg	gat	tac	aac	aac	atc	cca	acg	ctc	aac	aag	gcc		912

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser	Phe	Gln	Leu	Met	Asp	Tyr	Asn	Asn	Ile	Pro	Thr	Leu	Asn	Lys	Ala	
290					295						300					
atg	ttc	tgg	ggt	act	ctc	gtg	ggc	gag	ttt	atc	cct	acc	gcc	acg	gga	960
Met	Phe	Trp	Gly	Thr	Leu	Val	Gly	Glu	Phe	Ile	Pro	Thr	Ala	Thr	Gly	
305					310					315					320	
att	tgg	gaa	ttt	ggc	ctc	agt	gtc	ttt	ggc	act	gcc	gac	ctt	tat	att	1008
Ile	Trp	Glu	Phe	Gly	Leu	Ser	Val	Phe	Gly	Thr	Ala	Asp	Leu	Tyr	Ile	
					325				330					335		
gat	aat	gag	ctc	gtg	att	gaa	aat	aca	aca	cat	cag	acg	cgt	gga	acc	1056
Asp	Asn	Glu	Leu	Val	Ile	Glu	Asn	Thr	Thr	His	Gln	Thr	Arg	Gly	Thr	
					340			345					350			
gcc	ttt	tcc	gga	aag	gga	acg	acg	gaa	aaa	gtc	gct	acc	agg	agg	atg	1104
Ala	Phe	Phe	Gly	Lys	Gly	Thr	Thr	Glu	Lys	Val	Ala	Thr	Arg	Arg	Arg	Met
					355			360				365				
gtg	gcc	ggc	agc	acc	tac	aag	ctg	cgt	ctc	gag	ttt	ggg	tct	gcc	aac	1152
Val	Ala	Gly	Ser	Thr	Tyr	Lys	Leu	Arg	Leu	Glu	Phe	Gly	Ser	Ala	Asn	
					370		375				380					
acg	acc	aag	atg	gag	acg	acc	ggt	gtt	gtc	aac	ttt	ggc	ggc	ggt	gcc	1200
Thr	Thr	Lys	Met	Glu	Thr	Thr	Gly	Val	Val	Asn	Phe	Gly	Gly	Gly	Ala	
					385		390			395					400	
gta	cac	ctg	ggt	gcc	tgt	ctc	aag	gtc	gac	cca	cag	gag	atg	att	gcg	1248
Val	His	Leu	Gly	Ala	Cys	Leu	Lys	Val	Asp	Pro	Gln	Gl	Met	Ile	Ala	
					405			410					415			
cg	gcc	gtc	aag	gcc	gca	gcc	gat	gcc	gac	tac	acc	atc	atc	tgc	acg	1296
Arg	Ala	Val	Lys	Ala	Ala	Ala	Asp	Ala	Asp	Tyr	Thr	Ile	Ile	Cys	Thr	
					420			425				430				
gga	ctc	agc	ggc	gag	tgg	gag	tct	gag	ggt	ttt	gac	cgg	cct	cac	atg	1344
Gly	Leu	Ser	Gly	Glu	Trp	Glu	Ser	Glu	Gly	Phe	Asp	Arg	Pro	His	Met	
					435		440				445					
gac	ctg	ccc	cct	ggt	gtg	gac	acc	atg	atc	tcg	caa	gtt	ctt	gac	gcc	1392
Asp	Leu	Pro	Pro	Gly	Val	Asp	Thr	Met	Ile	Ser	Gln	Val	Leu	Asp	Ala	
					450		455			460						
gct	ccc	aat	gct	gta	gtc	aac	cag	tca	ggc	acc	cca	gtg	aca	atg		1440
Ala	Pro	Asn	Ala	Val	Val	Asn	Gln	Ser	Gly	Thr	Pro	Val	Thr	Met		
					465			470			475			480		
agc	tgg	gct	cat	aaa	gca	aag	gcc	att	gtg	cag	gct	tgg	tat	ggt	ggt	1488
Ser	Trp	Ala	His	Lys	Ala	Lys	Ala	Ile	Val	Gln	Ala	Trp	Tyr	Gly	Gly	
					485			490				495				
aac	gag	aca	ggc	cac	gga	atc	tcc	gat	gtg	ctc	ttt	ggc	aac	gtc	aac	1536
Asn	Glu	Thr	Gly	His	Gly	Ile	Ser	Asp	Val	Leu	Phe	Gly	Asn	Val	Asn	
					500			505				510				
ccg	tcg	ggg	aaa	ctc	tcc	cta	tcg	tgg	cca	gtc	gat	gtg	aag	cac	aac	1584
Pro	Ser	Gly	Lys	Leu	Ser	Leu	Ser	Trp	Pro	Val	Asp	Val	Lys	His	Asn	
					515			520				525				
cca	gca	tat	ctc	aac	tac	gcc	agc	gtt	ggt	gga	cgg	gtc	ttg	tat	ggc	1632
Pro	Ala	Tyr	Leu	Asn	Tyr	Ala	Ser	Val	Gly	Gly	Arg	Val	Leu	Tyr	Gly	
					530		535				540					

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gag gat gtt tac gtt ggc tac aag ttc tac gac aaa acg gag agg gag Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu 545 550 555 560	1680
gtt ctg ttt cct ttt ggg cat ggc ctg tct tac gct acc ttc aag ctc Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu 565 570 575	1728
cca gat tct acc gtg agg acg gtc ccc gaa acc ttc cac ccg gac cag Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln 580 585 590	1776
ccc aca gta gcc att gtc aag atc aag aac acg agc agt gtc ccg ggc Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly 595 600 605	1824
gcc cag gtc ctg cag tta tac att tcg gcc cca aac tcg cct aca cat Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His 610 615 620	1872
cgc ccg gtc aag gag ctg cac gga ttc gaa aag gtg tat ctt gaa gct Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala 625 630 635 640	1920
ggc gag gag aag gag gta caa ata ccc att gac cag tac gct act agc Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser 645 650 655	1968
ttc tgg gac gag att gag agc atg tgg aag agc gag agg ggc att tat Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gln Ile Tyr 660 665 670	2016
gat gtg ctt gta gga ttc tcg agt cag gaa atc tcg ggc aag ggg aag Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gln Lys Gly Lys 675 680 685	2064
ctg att gtg cct gaa acg cga ttc tgg atg ggg ctg tag Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gln Leu 700	2103

<210> 92
<211> 700
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct
<400> 92

Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
1 5 10 15

Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
20 25 30

Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
35 40 45

60110USPCT1 Corrected SEQ LIST 2-2007.txt
val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
50 55 60

val Asn Gly Lys His val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
65 70 75 80

Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile val Ser Asp Trp Tyr
85 90 95

Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
100 105 110

Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
115 120 125

Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
130 135 140

val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
145 150 155 160

Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
165 170 175

Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
180 185 190

Leu Pro Lys Ser Val Lys Val Ala Leu Val Gly Ser His Val Arg
195 200 205

Leu Pro Ala Ile Ser Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
210 215 220

Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
225 230 235 240

Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
245 250 255

Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
260 265 270

Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
275 280 285

Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
290 295 300

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305 310 315 320

Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
325 330 335

Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
340 345 350

Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
355 360 365

Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
370 375 380

Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385 390 395 400

Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
405 410 415

Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
420 425 430

Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
435 440 445

Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
450 455 460

Ala Pro Asn Ala Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465 470 475 480

Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
485 490 495

Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
500 505 510

Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
515 520 525

Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
530 535 540

Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545 550 555 560

60110USPCT1 Corrected SEQ LIST 2-2007.txt

val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
565 570 575

Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
580 585 590

Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
595 600 605

Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
610 615 620

Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625 630 635 640

Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
645 650 655

Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr
660 665 670

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
675 680 685

Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
690 695 700

<210> 93

<211> 1496

<212> DNA

<213> Artificial sequence

<220>

<223> Maize optimized CBHI

<400> 93

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tctgcccga caacgagacc tgcccaaga actgctgcct cgacggcgcc gcctacgcct 120
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cccagaagaa cgtggcgcc cgcctctacc tcatggcctc cgacaccacc taccaggagt 180
tcaccctcct cggcaacgag ttctccttcg acgtggacgt gtcccagctc ccgtgcggcc
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420
480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

ccaacaccgc	cgcgccaaag tacggcaccg gctactgcga ctcccagtgc ccgcgcgacc	540
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acaccggcat	cggcggccac ggctcctgct gctccgagat ggacatctgg gaggccaact	660
ccatctccga	ggccctcacc ccgcacccgt gcaccaccgt gggccaggag atctgcgagg	720
gcgacggctg	cggcggcacc tactccgaca accgctacgg cggcacctgc gacccggacg	780
gctgcgactg	gaacccgtac cgccctggca acacccctt ctacggcccg ggctcctcct	840
tcaccctcga	caccaccaag aagctcaccg tggtgaccga gttcgagacc tccggcgcca	900
tcaaccgcta	ctacgtgcag aacggcgtga cttccagca gccgaacgcc gagctcggt	960
cctactccgg	caacgagctc aacgacgact actgcacccgc cgaggaggcc gagttcgccg	1020
gctcctcctt	ctccgacaag ggcggcctca cccagttcaa gaaggccacc tccggcgca	1080
tggtgcttgt	gatgtccctc tgggacgact actacgccaa catgctctgg ctcgactcca	1140
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gcccgaccga	gtcccactac ggccagtgcg gcggcatcgg ctactccggc ccgaccgtgt	1440
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<210> 94
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized CBHII

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tactcccagt	gcctcccggt cgccgcctcc tcctcctccct ccacccgcgc cgcctccacc	180
acctcccgcg	tgtccccgac cacctccgc tcctcctccg ccacccgcc gcccggctcc	240
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gtgggcgtga	ccccgtggc caacgcctac tacgcctccg aggtgtcctc cctcgccatc	360
ccgtccctca	ccggcgccat ggccaccgccc gcccgcgcg tggccaaggt gccgtccttc	420
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accgccaaca	agaacggcgg caactacgccc ggccagttcg tggtgacgaa cctccggac	540
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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cactgcgccc tcccggacgc cctccagccg gccccgcagg ccggcgctg gttccaggcc 1320
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<210> 95
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized EGLI

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tggatgcacg acgccaacta caactcctgc accgtgaacg gcggcgtaa caccaccctc
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tccggcgta ccaccc 300
ctccctcc accatgaacc agtacatgcc gtcctcc
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420
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aggacgaga acggcgccgc caaccgtac
aacaccgcg gcgccaacta cggctccggc tactgcacg cccagtgc 540
ggcgcaacg gcaccctcaa caccc 600
cccac cagggtttct gctgcaacga gatggacatc
ctcgagg 660
ggcgcgc 720
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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tggAACGACA	actcccagta	catgaactgg	ctcgactccg	gcaacgccgg	cccgtgctcc	1020
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tccaaacatcc	gctggggcga	catcggtcc	accaccaact	ccaccgcccc	gccgcccgg	1140
ccggcctcct	ccaccacctt	ctccaccacc	cggcgtcct	ccaccaccc	ctcctccccg	1200
tcctgcaccc	agacccactg	gggccagtgc	ggcggcatcg	gctactccgg	ctgcaagacc	1260
tgcacctccg	gcaccacctg	ccagtagtcc	aacgactact	actcccagtg	cctctag	1317

<210> 96
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized BGLII

<400> 96

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atcgccgacg	gctcctccgg	cgtgaccgccc	tgcactcct	acaaccgcac	cggcggaggac	180
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aagttcgtgg	acgacccct	cgacgcccgc	atcacccgt	tcatcaccct	cttccactgg	360
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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gtgaccgccc tggagctcga cggcgtgaac gtgaaggct acttcgcctg gtccctcatg	1260
gacaacttcg agtgggcccga cggctacgtg acccgcttcg gcgtgaccta cgtggactac	1320
gagaacggcc agaagcgctt cccgaagaag tccgccaagt ccctcaagcc gctttcgac	1380
gagctcatcg ccgcccgccta g	1401

<210> 97
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized CEL3D

<400> 97 atgatcctcg gctgcgagtc caccggcgtg atctccgccc tgaagcactt cgtggccaac	60
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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gagggcttcg	accgcccga	catggacctc	ccgcccggcg	tggacaccat	gatctccag	1380
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tag						2103

<210> 98
<211> 420
<212> DNA
<213> Zea mays

<220>
<223> Q protein promoter

<400> 98
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ctagttgtca caagttgtat atcgattcgt cgcgtttcaa caactcatgc aacattacaa
acaagtaaca caatattaca aagttatctt catacaaagc aagaaaagga caataatact
tgacatgtaa agtgaagctt attatacttc ctaatccaac acaaaaacaaa aaaaagttgc 240
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attatccaaac aaatgtttat caatgtggta tcataacaagc attgacatcc cataaatgca 300
agaaaattgtg ccaacaaagc tataagtaac cctcatatgt atttgcactc atgcatacaca 360
420

<210> 99
<211> 1188
<212> DNA
<213> artificial sequence

<220>

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<223> synthetic ferulic acid esterase

<400> 99

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<210> 100

<211> 395

<212> PRT

<213> artificial sequence

<220>

<223> synthetic ferulic acid esterase

<400> 100

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Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
20 25 30

Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly

35

60110USPCT1 Corrected SEQ LIST 2-2007.txt
40
45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
50 55 60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Arg Ala Asn Val
65 70 75 80

Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
85 90 95

Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
100 105 110

Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
115 120 125

Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
130 135 140

Leu Ser Met Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
145 150 155 160

Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
165 170 175

Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
180 185 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
195 200 205

Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
210 215 220

Val Tyr Trp Leu Ile Gln Gly Gly His Asp Phe Asn Val Trp Lys
225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

60110USPCT1 Corrected SEQ LIST 2-2007.txt
Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 101
<211> 1188
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13036

<400> 101
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gtgttcaagg gcccggtgaa catcgactgg ttcaccttcg gcgtgttag 1188

<210> 102
<211> 395
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 13036

<400> 102

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Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
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Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
35 40 45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
50 55 60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Arg Ala Asn Val
65 70 75 80

Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
85 90 95

Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
100 105 110

Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
115 120 125

Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
130 135 140

Leu Ser Met Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
145 150 155 160

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
165 170 175

Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
180 185 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
195 200 205

Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
210 215 220

Val Tyr Trp Leu Ile Gln Gly Gly His Asp Phe Asn Val Trp Lys
225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<211> 1245

<212> DNA

<213> artificial sequence

<220>

<223> plasmid 13038

<400> 103

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cgcggccagg tggtaaacat ctccctacttc tccaccgcca ccaactccac ccgcccggcc 180
cgcgtgtacc tcccgcggg ctactccaag gacaagaagt actccgtgct ctacccctc 240
cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
gccgacaacc tcattcgccga gggcaagatc aagccgctca tcattgtgac cccgaacacc 360
aacggcccg gcccggcat cgccgacggc tacgagaact tcaccaagga cctccctcaac 420
tccctcatcc cgtacatcga gtccaaactac tccgtgtaca ccgaccgcga gcaccgcgc 480
atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 540
aagttcgctt acatcgcccc gatctccgccc gccccgaaca cctaccgaa cgagcgcctc 600
ttcccgacg gcggcaaggc cgccccgcag aagctcaagc tcctcttcat cgcctgcggc 660
accaacgact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720
atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaaagccg 780
ggcctctgga acttcctcca gatggccac gaggccggcc tcacccgcga cggcaacacc 840
ccggtgccga ccccgccccc gaagccggcc aacacccgca tcgaggccga ggactacgac 900
ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 960
ggctacatca cctccggcga ctacctcggt tacaagtcca tcgacttcgg caacggcgcc 1020
accccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080
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tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgaccc ctacctcggt 1200
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<210> 104

<211> 414

<212> PRT

<213> artificial sequence

<220>

<223> plasmid 13038 aa

<400> 104

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Arg
85 90 95

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gln Ser Phe Asn Ile Gly Leu
165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly His Asp Phe Asn
245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
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260

60110USPCT1 Corrected SEQ LIST 2-2007.txt
265
270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
405 410

<210> 105

<211> 1425

<212> DNA

<213> artificial sequence

<220>

<223> plasmid 13039

<400> 105

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gcggcggaca cgctcagcat gcggaccaggc gcgcgcgcgg cgcccaggca ccagcaccagg 180

caggcgcgcc gcggggccag gttcccgtcg ctcgtcgtgt gcgcgcgcgc cgccgcgcattg 240

gccgcctccc tcccgaccat gccgcgtcc ggctacgacc aggtgcgcaa cggcggtgccg 300

cgccggccagg tggtgaacat ctcctacttc tccaccgcca ccaactccac ccgcggccgc 360

cgctgttacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctaccccttc 420

cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gccgacaacc	tcatcgccga	gggcaagatc	aagccgctca	tcatcgac	cccgaacacc	540
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tccctcatcc	cgtacatcga	gtccaaactac	tccgtgtaca	ccgaccgcga	gcaccgcgcc	660
atcgccggcc	tctctatggg	cggcggccag	tccttcaaca	tcggcctcac	caacctcgac	720
aagttcgct	acatcgcccc	gatctccgcc	gccccgaaca	cctacccgaa	cgagcgcctc	780
ttcccgacg	gcccgaaggc	cggccgcgag	aagctcaagc	tcctttcat	cgcctgcggc	840
accaacgact	ccctcatcg	ttcggccag	cgcgtgcacg	agtactgcgt	ggccaacaac	900
atcaaccacg	tgtactggct	catccaggc	ggcggccacg	acttcaacgt	gtggaagccg	960
ggcctctgga	acttcctcca	gatggccgac	gaggccggcc	tcacccgcga	cggcaacacc	1020
ccgggtgccg	ccccgtcccc	gaagccggcc	aacacccgca	tcgaggccga	ggactacgac	1080
ggcatcaact	cctcctccat	cggatcatc	ggcgtgccgc	cggaggcgg	ccgcggcatc	1140
ggctacatca	cctccggcga	ctacctcg	tacaagtcca	tcgacttcgg	caacggcgcc	1200
acctccttca	aggccaaggt	ggccaacgcc	aacaccccca	acatcgagct	tcgcctcaac	1260
ggcccgaacg	gcaccctcat	cggcaccctc	tccgtgaagt	ccaccggcga	ctggaacacc	1320
tacgaggagc	agacctgctc	catctccaag	gtgaccggca	tcaacgacct	ctacctcg	1380
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<210> 106

<211> 474

<212> PRT

<213> artificial sequence

<220>

<223> plasmid 13039 aa

<400> 106

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1 5 10 15

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20 25 30

Leu Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg
35 40 45

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50 55 60

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65 70 75 80

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val Arg
85 90 95

Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser Thr
100 105 110

Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly Tyr
115 120 125

Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile Gly
130 135 140

Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Arg Ala Asn Val Ile
145 150 155 160

Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile Val
165 170 175

Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr Glu
180 185 190

Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu Ser
195 200 205

Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly Leu
210 215 220

Ser Met Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu Asp
225 230 235 240

Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr Pro
245 250 255

Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys Leu
260 265 270

Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly Phe
275 280 285

Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His Val
290 295 300

Tyr Trp Leu Ile Gln Gly Gly His Asp Phe Asn Val Trp Lys Pro
305 310 315 320

Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr Arg
325 330 335

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn Thr
340 345 350

Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile Glu
355 360 365

Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile Thr
370 375 380

Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly Ala
385 390 395 400

Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile Glu
405 410 415

Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser Val
420 425 430

Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser Ile
435 440 445

Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly Pro
450 455 460

Val Asn Ile Asp Trp Phe Thr Phe Gly Val
465 470

<210> 107

<211> 1263

<212> DNA

<213> artificial sequence

<220>

<223> plasmid 13347

<400> 107

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gccgcctccc tcccgaccat gccgcgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120

cgcggccagg tggtaaacat ctcctacttc tccaccgcca ccaactccac ccgccccggcc 180

cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacccctc 240

cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300

gccgacaacc tcatacgccga gggcaagatc aagccgctca tcatacggtac cccgaacacc 360

aacgcccggc gcccgggcat cgccgacggc tacgagaact tcacccaagga cctccctcaac 420

tccctcatcc cgtacatcga gtccaaactac tccgtgtaca ccgaccgcga gcaccgcgc 480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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aagttgcct acatcgcccc gatctccgcc gccccgaaca cctaccgaa cgagcgcc 600
ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tccttcat cgcctgcggc 660
accaacgact ccctcatcg cttcgccag cgctgtcacg agtactgcgt ggccaacaac 720
atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780
ggcctctgga acttcctcca gatggccgac gaggccggcc tcacccgca cggcaacacc 840
ccgggtgccga ccccgccccc gaagccggcc aacacccgca tcgaggccga ggactacgac 900
ggcatcaact ctcctccat cgagatcatc ggctgtccgc cggagggcgg ccggccatc 960
ggctacatca ctcggcga ctacctcgta tacaagtcca tcgacttcgg caacggcgcc 1020
acctccttca aggccaaggt ggccaacgccc aacaccccca acatcgagct tcgcctcaac 1080
ggcccgaacg gcaccctcat cggcaccctc tccgtgaagt ccaccggcga ctggAACACC 1140
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgta 1200
ttcaaggccc cggtgaacat cgactggttc accttcggcg tgtccgagaa ggacgaactc 1260
tag 1263

<210> 108

<211> 420

<212> PRT

<213> artificial sequence

<220>

<223> plasmid 13347

<400> 108

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

·Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Arg
85 90 95

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gln Ser Phe Asn Ile Gly Leu
165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
195 200 205

Arg Glu Lys Leu Lys Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly His Asp Phe Asn
245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
260 265 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
340 345 350

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val Ser Glu
405 410 415

Lys Asp Glu Leu
420

<210> 109

<211> 1296

<212> DNA

<213> artificial sequence

<220>

<223> plasmid 11267

<400> 109

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cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccggacgc ctggccgacc 180

tggccggta agctcggcga gctgaccccg cgccggccgc agctgatcgc ctacctcggc 240

cactactggc gccagcgcct cgtggccgac ggcctcctcc cgaagtgcgg ctgcccgcag 300

tccggccagg tggccatcat cgccgacgtg gacgagcgc cccgcaagac cggcgaggcc 360

ttcgccgccc gcctcgcccc ggactgcgcc atcaccgtgc acacccaggc cgacacctcc 420

tccccggacc cgctttcaa cccgctcaag accggcgtgt gccagctcga caacgccaac 480

gtgaccgacg ccatccttggaa gcgcgcccggc ggctccatcg ccgacttcac cggccactac 540

cagaccgcct tcccgagact ggagcgcgtg ctcaacttcc cgcagtccaa cctctgcctc 600

aagcgcgaga agcaggacga gtcctgctcc ctcacccagg ccctccgtc cgagctgaag 660

gtgtccgccc actgcgtgtc cctcaccggc gccgtgtccc tcgcctccat gtcaccgaa 720

atttcctcc tccagcaggc ccagggcatg ccggagccgg gctggggccg catcaccgac 780

tcccaccagt ggaacaccct cctctccctc cacaacgccc agttcgacct cctccagcgc 840

accccgagg tggcccgctc ccgcgcacc ccgctcctcg acctcatcaa gaccgcctc 900

accccgacc cgccgcagaa gcaggcctac ggcgtgaccc tcccgacctc cgtgctttc 960

atcgccggcc acgacaccaa cctcgccaaac ctcggcggcg ccctggagct gaactggacc 1020

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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cgccctctccg acaactccca gtggattcag gtgtccctcg tttccagac cctccagcag 1140
atgcgcgaca agaccccgct ctccctcaac accccgcccgg gcgaggtgaa gtcaccctc 1200
gccggctgctgaggagcgcaa cgcccagggc atgtgctccc tcgcccggctt cacccagatc 1260
gtgaacgagg cccgcatccc gcctgctcc ctctaa 1296

<210> 110
<211> 431
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 11267 aa sequence

<400> 110

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20 25 30

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35 40 45

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50 55 60

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65 70 75 80

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
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165 60110USPCT1 Corrected SEQ LIST 2-2007.txt
170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
225 230 235 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

60110USPCT1 Corrected SEQ LIST 2-2007.txt
Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
420 425 430

<210> 111
<211> 1314
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 11268

<400> 111
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cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccggacgc ctggccgacc 180
tggccggta agctcggcga gctgaccccg cgccggcggcg agctgatcgc ctacctcgac 240
cactactggc gccagcgcct cgtggccgac ggcctcctcc cgaagtgcgg ctgcccgcag 300
tccggccagg tggccatcat cgccgacgtg gacgagcgc cccgcaagac cggcgaggcc 360
ttcgccgccc gcctcgcccc ggactgcgcc atcaccgtgc acacccaggc cgacacctcc 420
tccccggacc cgctcttcaa cccgctcaag accggcgtgt gccagctcga caacgccaac 480
gtgaccgacg ccatcctgga gcgcgcggc ggctccatcg ccgacttcac cggccactac 540
cagaccgcct tccgcgagct ggagcgcgtg ctcaacttcc cgcagtc当地 cctctgcctc 600
aagcgcgaga agcaggacga gtcctgctcc ctcacccagg ccctccgtc cgagctgaag 660
gtgtccgccc actgcgtgtc cctcaccggc gccgtgtccc tcgcctccat gtcaccgaa 720
atcttcctcc tccagcaggc ccagggcatg ccggagccgg gctggggccg catcaccgac 780
tcccaccagt ggaacaccct cctctccctc cacaacgc当地 agttcgacct cctccagcgc 840
accccgagg tggccgctc ccgcgc当地 accgcctcg acctcatcaa gaccgc当地 900
accccgacc cgccgc当地 aa gcaggcctac ggcgtgaccc tcccgacctc cgtgctttc 960
atgcgc当地 acgacaccaa cctcgccaaac ctcggcggcg ccctggagct gaactggacc 1020
ctcccgccc agccggacaa caccggccg ggcggc当地 tgggtttcga ggc当地ggcgc 1080
cgccctctccg acaactccca gtggatttag gtgtccctcg tggccagac cctccagcag 1140
atgcgc当地 agacccgct ctc当地caac accggccgg gcgaggtgaa gtc当地ccctc 1200
gccggctgcn aggagcgc当地 cgcccgaggc atgtgctccc tcgc当地ggctt cacccagatc 1260
gtgaacgagg cccgcatccc ggc当地gtcc ctc当地ccgaga aggacgagct gtaa 1314

<210> 112
<211> 437
<212> PRT
<213> artificial sequence

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<223> plasmid 11268 amino acid sequence

<400> 112

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20 25 30

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35 40 45

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50 55 60

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65 70 75 80

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
225 230 235 240

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Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Ser
420 425 430

Glu Lys Asp Glu Leu
435